

A:Molecule type: DNA
A:Residues: 1-269 -SGL-

A:Cross-references: EMBL:AF083573, SFL:4759194, FILL:AA362739.1

Query Match 96.8% Score 40; DB 2; Length 269;

Best Local Similarity 84.3% Prod. No. 14;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQRRGR 6

|||||

DB 55 LQRRGR 60

RESULT 8

T09701

C:Species: Pinus sylvestris (Scotch pine)

C:Date: 16 Jul 1999 #sequence revision 16-Jul 1999 #text change 20-Jun-2000

C:Accession: T09701

R:Wisniamski-Rund, C.M.; Kolukisaoglu, H.O.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z16826

C:Accession: T09701

A:Status: Preliminary; translated from 32/2584/T096

A:Molecule type: mRNA

A:Residues: 1-114 -WLE-

A:Cross-references: EMBL:X96738; MID:q1247803

A:Experimental source: Isolate TSA 5.1

C:Superfamily: phytochrome; phytochrome homology

C:Keywords: chromoprotein; photoreceptor; phytochromobilin

F:75-5879/wmat; phytochrome homology - PHY

F:432/6/fidat site; phytochromobilin (75) (conserved) #status Predicted

Query Match

Best Local Similarity 96.8% Score 30; DB 2; Length 114;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQRRGR 6

|||||

DB 82 LQRRGR 87

RESULT 9

B69156

hypothetical protein MTH430 - Methanobacterium thermotum raphicum (strain delta B)

C:Species: Methanobacterium thermotum raphicum

C:Date: 05 Dec 1997 #sequence 16-Sep-95 16-Sep-97 #text change 22-Nov-1998

C:Accession: B69156

R:Smith, D.R.; Doucette-Stamm, L.A.; Delouche, C.; Lee, H.; Hubbell, J.; Aldredge, T.

Qiu, D.; Spadator, R.; Vicat, K.; Wais, T.; Wierzbowski, J.; Gibbons, R.; Liwanag, N.

Church, G.M.; Daniels, G.J.; Moir, J.; Rhee, P.; Neill, J.; Reece, J.R.

Bacteriol. 179, 7145-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermotum raphicum delta B: tunc

A:Reference number: A69000; MUID:98047514

C:Accession: B69156

A:Status: Preliminary; nucleic acid sequence and abseq. translation not shown

A:Molecule type: DNA

A:Residues: 1-134 -MTH-

A:Cross-references: EMBL:AF093827, CP:AF093827, M1242621459, FILL:MAE3799.1, FILL:4252147

A:Experimental source: strain delta B

C:Keywords:

A:Gene: MTH430

A:Start codon: TTG

Query Match

Best Local Similarity 90.3% Score 28; DB 2; Length 134;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQRRGR 6

|||||

DB 108 LQRRGR 114

RESULT 10

S69652

actin-like protein Xp-16434 [imported] Pseudomonas aeruginosa

C:Species: Pseudomonas aeruginosa

C:Date: 13 Jan 1995 #sequence revision 13-Jan 1995 #text change 01-Dec 2000

C:Accession: S69652; B04268

R:Kobayashi, M.; Balle, M.; Ball, T.; Marston, J.; Tacke, E.; Filler, A.; Landau, K.

Mol. Microbiol. 10, 431-444, 1994

A:Title: Xp-mediated protein secretion in Pseudomonas aeruginosa: identification of

A:Reference number: S69652; MUID:95020542

C:Accession: S69652

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-255 -AKK-

R:Stoyan, C.K.; Pham, X.Q.; Erwin, A.L.; Mitsuuchi, S.D.; Warren, P.; Hickey, M.L.

Am. J. Path. 133, 133-140, 1993

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunist

A:Reference number: A62950; MUID:20447447

C:Accession: B04268

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-230 -STP-

A:Cross-references: EMBL:AF044741, GEM:AF044741, M1242621459, FILL:AA36396.1, FILL:BB3

A:Experimental source: strain PA01

C:Keywords:

A:Gene: xpp1; PA-104

Query Match

Best Local Similarity 95.0% Score 28; DB 2; Length 255;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQRRGR 6

|||||

DB 104 LQRRGR 159

RESULT 11

B04462

probable short chain dehydrogenase PA1470 [imported] Pseudomonas aeruginosa (strain

C:Species: Pseudomonas aeruginosa

C:Date: 15 Sep 2000 #sequence revision 15-Sep 2000 #text change 03-Aug 2001

C:Accession: B04462

R:Stoyan, C.K.; Pham, X.Q.; Erwin, A.L.; Mitsuuchi, S.D.; Warren, P.; Hickey, M.L.

Am. J. Path. 133, 133-140, 1993

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunist

A:Reference number: A62950; MUID:20447447

C:Accession: B04462

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-245 -STP-

A:Cross-references: EMBL:AF044741, GEM:AF044741, M1242621459, FILL:AA36396.1, FILL:BB3

A:Experimental source: strain PA01

C:Keywords:

C:Superfamily: short chain dehydrogenase; short chain dehydrogenase homology

Query Match

Best Local Similarity 84.0% Score 28; DB 2; Length 245;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQRRGR 6

|||||

DB 109 VERGRGR 154

RESULT 12

B00191

conserved hypothetical protein y71A Bacillus subtilis

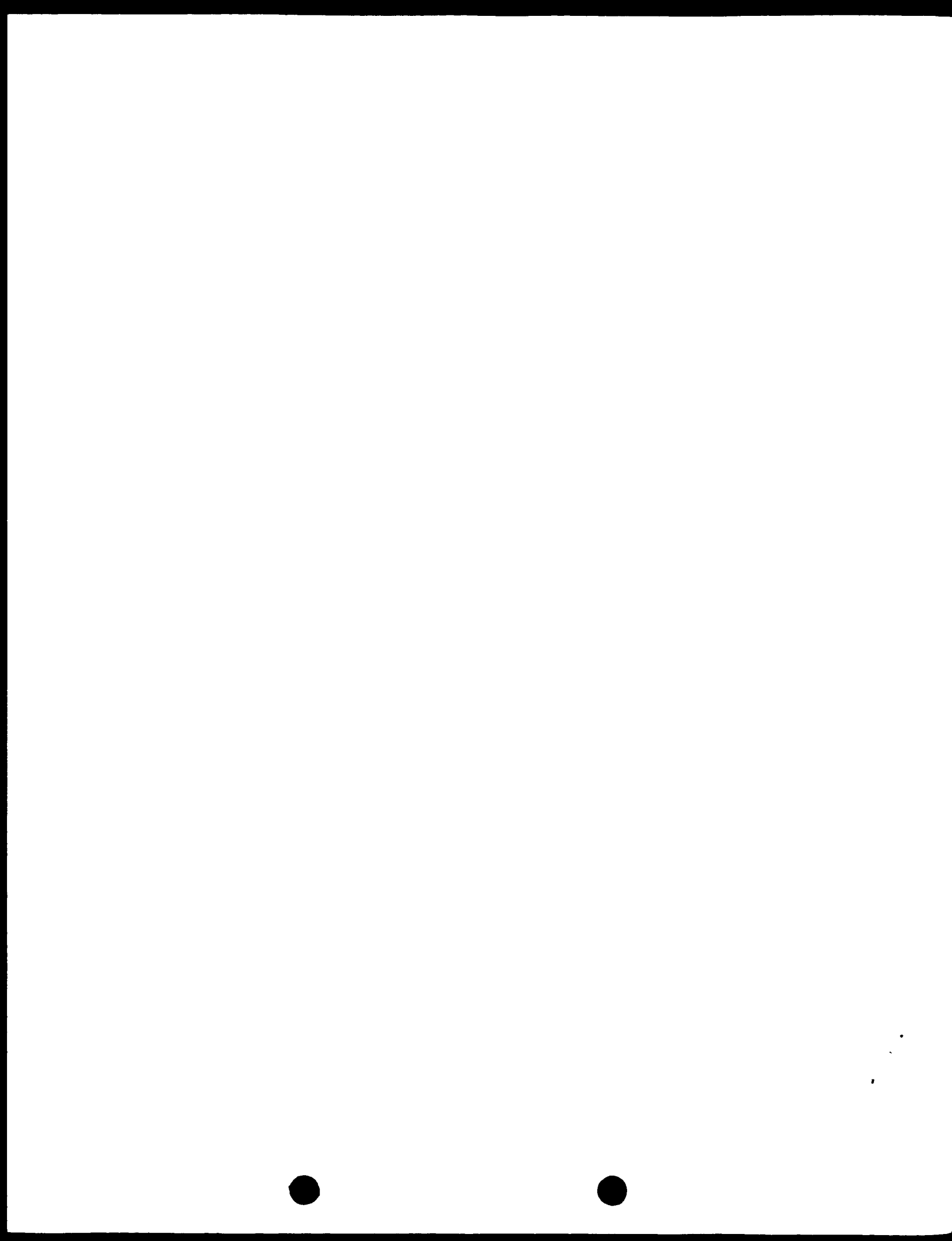
C:Species: *Bacillus subtilis*
 C:Date: 15-Oct-1999 #sequence_revision 15-sect-1999 #text_change 21-Jul-2000
 C:Accession: 140386; D30191; A70042; S28996
 P:Garcia-Vallejo, J.A.; Dubnau, D.
 Mol. Microbiol. 9, 119-131, 1994
 A:Title: comp. a *Bacillus subtilis* late competence locus, encodes a protein similar to A
 A:Reference number: 140386; M010:94018599
 A:Accession: 140386
 A:Molecule type: DNA
 A:Residues: 1-281 <RES>
 A:Cross references: EMBL:219629; NID:879847; FID:CAA79225.1; FID:a9848
 R:Henner, D.J.; Yang, M.; Ferrarini, E.
 J. Bacteriol. 170, 5102-5109, 1988
 A:Title: Localization of *Bacillus subtilis* *argW* mutations to two linked genes with A
 A:Reference number: A30191; M010:84034891
 A:Accession: D30191
 A:Molecule type: rRNA
 A:Residues: 1-107 <RES>
 P:Funf, P.; Ogasawara, N.; Messer, J.; Albertini, A.M.; Alloni, G.; Accardo, V.; Berter
 A.; Bron, S.; Rouillet, S.; Brusch, C.V.; Caldwell, R.; Capuano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fahrel, G.; Ferrarini, E.
 Nature 340, 249-256, 1997
 A:Authors: Rouget, D.; Fritz, G.; Fujita, M.; Fujita, Y.; Fujita, S.; Gailard, A.; Gail
 A.; Harwood, C.P.; Hebut, A.; Hiltner, E.; Hiltner, S.; Hiltner, S.; Hiltner, M.P.
 Koehler, P.; Koningstein, G.; Krog, S.; Krog, S.; Krog, S.; Krog, S.; Krog, S.; Krog, S.
 A:Authors: Lauber, J.; Lavareto, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
 Y.M.; Ogasawa, K.; Ogasawa, K.; Ogasawa, K.; Ogasawa, K.; Ogasawa, K.; Ogasawa, K.
 Rieger, M.; Rieger, M.; Rieger, M.; Rieger, M.; Rieger, M.; Rieger, M.; Rieger, M.
 A:Authors: Schleich, S.; Schleich, S.; Schleich, S.; Schleich, S.; Schleich, S.; Schleich, S.
 A.; Tamaki, M.; Tamaki, M.; Tamaki, M.; Tamaki, M.; Tamaki, M.; Tamaki, M.; Tamaki, M.
 I.; Winters, F.; Winters, F.; Winters, F.; Winters, F.; Winters, F.; Winters, F.; Winters, F.
 A:Authors: Yoshikawa, H.; Yoshikawa, H.; Yoshikawa, H.; Yoshikawa, H.; Yoshikawa, H.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*
 A:Reference number: A69580; M010:98044033
 A:Accession: A70042
 A>Status: nucleic acid sequence not shown, translation not shown
 A:Molecule type: DNA
 A:Residues: 1-281 <RES>
 A:Cross references: GB:209122; GB:AL039136; M010:4264029; FID:CA815565.1; FID:a2646074
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: *viaA*
 C:Superfamily: Mycoplasma hypothetical protein MG326

Query Match 90.4% Score 29, 17 Length 281
 Best Local Similarity 83.3% Pred. No. 20+02
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0
 QY 1 VORGER 6
 DB 167 LORGER 172
 RESULT 13
 ABL389
 B. subtilis *viaA* (gen) protein homolog lin2658 [imported] - *Listeria innocua* (strain
 C:Species: *Listeria innocua*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: A01764
 P:Domínguez-Bernal, G.; Durand, E.; Durand, E.; Durand, E.; Durand, E.; Durand, E.; Durand, E.
 A.; Domínguez-Bernal, G.; Durand, E.; Durand, E.; Durand, E.; Durand, E.; Durand, E.; Durand, E.
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Krell, T.; Krell, T.; Krell, T.; Krell, T.; Krell, T.; Krell, T.; Krell, T.
 A.; Krell, T.; Krell, T.; Krell, T.; Krell, T.; Krell, T.; Krell, T.; Krell, T.
 A:Title: Comparative genomics of *Listeria* species
 A:Reference number: A01077; M010:21537279; PMID:11679669
 A:Accession: A01764
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-281 <GLA>
 A:Cross references: GB:AL039136; FID:CA815565.1; FID:a2646074
 A:Experimental source: strain 6111302
 C:Genetics:
 A:Gene: *lin2658*

Query Match 90.4% Score 29, 17 Length 281
 Best Local Similarity 83.3% Pred. No. 20+02
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0
 QY 1 VORGER 6
 DB 167 LORGER 172
 RESULT 15
 A48561
 Inner capsid protein VP6 bluetongue virus (serotype 11, strain USA)
 C:Species: bluetongue virus
 C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 17-Feb-1994
 C:Accession: A48561
 P:Rehman, G.T.; Chou, J.F.; Yang, Y.Y.; Li, J.K.
 Virus Res. 24, 415-424, 1992
 A:Title: Comparative sequence analyses of the complete structural protein VP6 genes of
 A:Reference number: A48561; M010:94034709
 A:Accession: A48561
 A:Molecule type: structural RNA
 A:Residues: 1-125 <SHWA>
 A:Cross references: GB:AL039136; FID:CA815565.1; FID:a2646074
 C:Genetics:
 A:Map position: assignment 9
 C:Superfamily: bluetongue virus VP6 protein
 C:Keywords: capsid protein

Query Match 90.4% Score 29, 17 Length 281
 Best Local Similarity 83.3% Pred. No. 20+02
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0
 QY 1 VORGER 6
 DB 167 LORGER 172
 Search completed: October 22, 2002, 16:03:24

Job time : 4.07421 secs



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om protein protein search, using sw model

Run on: October 22, 2002, 16:00:01 : Search time 0.508929 seconds
(x10000 alignments)
456,483 Million cell updates/sec

Title: US 09-996,748-8
Perfect score: 41
Sequence: 1 V06038 6

Scoring table: RLSDM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 4871950 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot_40: *

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	41	100.0	567	MOE1_SCHPO	094246 schizosar
2	41	100.0	1151	ITAI_HUMAN	p56199 homo sapin
3	40	96.8	1131	PHY_PINSY	q31417 pins sy
4	38	93.3	235	GSPN_PSEAE	q51575 pseudomada
5	28	90.3	281	DEGV_BACSD	p12436 bacillus su
6	28	90.3	325	V16_BTV11	p12933 bluetongue
7	28	90.3	325	V16_BTV12	p12934 bluetongue
8	28	90.3	325	V16_BTV17	p12935 bluetongue
9	28	90.3	329	V161_BTV10	p23066 bluetongue
10	28	90.3	376	KITH_HSV23	p04407 herpes simp
11	28	90.3	550	P1N1_PDS371	p12944 desulfofytir
12	28	90.3	892	ENV_31VH1	p05885 simian immu
13	27	87.1	88	K115_BRANA	p46289 brassica na
14	27	87.1	153	K115_PIG	p79324 sus scrofa
15	27	87.1	174	K115_PARS1	p25432 oryctolagus
16	27	87.1	165	K115_CHICK	p51417 gallus gall
17	27	87.1	173	PR13_RANCA	p07797 bos taurus
18	27	87.1	174	PR13_BOVIN	p46415 bos taurus
19	27	87.1	174	PR13_HORSE	p02791 equus cabal
20	27	87.1	174	PR13_HUMAN	p02792 homo sapin
21	27	87.1	174	PR13_RABIT	p07451 oryctolagus
22	27	87.1	177	PR13_SALSA	p09946 salmo salar
23	27	87.1	179	PR13_CHICK	p08267 gallus gall
24	27	87.1	180	PR13_BOVIN	p46414 bos taurus
25	27	87.1	181	PR13_MOUSE	p09928 mus musculu
26	27	87.1	181	PR13_RAT	p19132 rattus norv
27	27	87.1	182	PR13_HUMAN	p02794 homo sapin
28	27	87.1	182	PR13_TRITU	q9x173 trichostema
29	27	87.1	182	SRPB_SYNE7	q55026 synchocoe
30	27	87.1	185	PR13_CRIER	p29489 cricetus
31	27	87.1	194	K15E_PVRAB	q92042 pyruococcus
32	27	87.1	194	K15E_PVRAB	q58706 pyruococcus
33	27	87.1	201	RL15_SCHPO	q74495 schizosar

41 27 87.1 203 1 RL15_ASPIG
45 27 87.1 203 1 RL15_WHITE
46 27 87.1 203 1 RL15_BHRAN
47 27 87.1 204 1 RL15A_PICMA
48 27 87.1 204 1 RL15B_PICMA
49 27 87.1 204 1 RL15_APAATH
40 27 87.1 204 1 RL15_DROME
41 27 87.1 204 1 RL15_PETHY
42 27 87.1 214 1 RL15_MOUSE
43 27 87.1 265 1 H1_PEA
44 27 87.1 329 1 K131_VIRRH
45 27 87.1 390 1 G000_MYC10

ALIGNMENTS

RESIDUE
MOE1_SCHPO
ID MOE1_SCHPO STAMARD PPT: 6.7 AA.
AA 094246
DT 30 MAY 2000 (Rel. 09, Created)
DT 30 MAY 2000 (Rel. 09, Last sequence update)
DE Microtubule destabilizing protein moe1.
GN MOE1 OR SW637.07.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID 4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE 99119922; PubMed 9902665;
RA Chen C, Re L, Ye C, Chen J, Ben M, C, Papadaki P, Chant E.C.;
RT "Xia", a conserved protein in Schizosaccharomyces pombe, interacts
RT with a Ras effector, Sed1, to affect proper spindle formation.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:517-522(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN 9722;
RA Parrella R, Goffeau A, Wood V, Rajandream M.A., Barrell R.G.;
RT "Xia" (a conserved protein in Schizosaccharomycetes).
RT FUNCTION: PUTATIVE NEGATIVE REGULATOR FOR MICROTUBULE DYNAMICS.
RT INTERACTS: INTERACTS WITH SED1.
RT SUBUNIT: INTERACTS WITH SED1.
RT SUBCELLULAR LOCATION: Nucleus.
RT SIMILARITY: BELONGS TO THE EFAS7 FAMILY.

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DR EMBL AF040608; AA008943;
LR EMBL AF040608; CAA22586.1;
KW Nucleic protein.
FT COMPATIBLE 367
SQ SEQUENCE 6.7 AA: 6246 MW: 636267.47474747 CRR04;

Query Match 100.00; Score 41; Length 667;
Best Local Similarity 100.00; Prod. No. 26;
Mismatches 0; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 V06038 6

14 125 V06038 140

RESIDUE

ITAL_HUMAN	
ID	ITAL_HUMAN
AC	STANDARD; PRT: 1151 AA.
AD	P56199;
DT	01-NOV-1997 (rel 35, created)
DT	01-NOV-1997 (rel 35, last sequence update)
DT	01-NOV-2002 (rel 41, last annotation update)
DE	Integrin alpha-1 (Laminin and collagen receptor) (VIA 1) (VIA4a).
GN	ITGA1.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	MIM:192968;
OX	NCBI_Taxid:9606;
PN	[1]
RP	SEQUENCE FROM N.A.
RP	MEMLINE-93155124; PubMed 8428073;
RP	Briesewitz R, Epstein M.R, Marcantonio E.E;
RT	"Expression of native and truncated forms of the human integrin alpha-1 subunit";
CC	J. Biol. Chem. 268:12989-2996(1993);
CC	-1- FUNCTION: INTEGRIN ALPHA 1/BETA 1 IS A SPECIFIC FIBRININ AND COLLAGEN. IT RECOGNIZES THE FIBRINE HYDROXYLATED RESIDUE OF THE E-R IN COLLAGEN.
CC	-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-1 ASSOCIATES WITH BETA-1.
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-1- DOMAIN: THE INTEGRIN I-1 DOMAIN (RESIDY 125-436) IS A VWFA DOMAIN. CHANGES WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
CC	-1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
CC	-1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
CC	-1- SIMILARITY: CONTAINS 7 EG-GAP REPEATS.
CC	-1- DATABASE: NAME-PROW; NOTE=CD guide c0449a entry;
CC	WWW: "http://www.ncbi.nlm.nih.gov/ncbi-cdd/c0449a.html".
DR	HSSP: "http://www.ncbi.nlm.nih.gov/ncbi-cdd/c0449a.html".
DR	MIM: 192968;
DR	InterPro: IPR000413; Integrin_alpha.
DR	InterPro: IPR002035; VWFA.
DR	Pfam: PF01839; EG-GAP; 5.
DR	Pfam: PF00457; Integrin_A; 1.
DR	Pfam: PF00092; vwa; 1.
DR	PRINTS: PF00453; VWFADOMAIN.
DR	SMART: SM00191; Int_alpha; 5.
DR	SMART: SM00427; VWA; 1.
DR	PROSITE: PS00242; INTEGRIN_ALPHA; 1.
DR	PROSITE: PS0234; VWFA; 1.
KW	Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
KW	Repeat; Calcium; Magnesium.
FT	DOMAIN 1 3113
FT	TRANSMEM 1114 1146
FT	DOMAIN 1137 1151
FT	REPEAT 16 75
FT	REPEAT 2 75
FT	REPEAT 3 75
FT	DOMAIN 147 360
FT	REPEAT 349 404
FT	REPEAT 405 457
FT	REPEAT 459 520
FT	REPEAT 540 599
FT	REPEAT 602 654
FT	CA_BIND 470 478
FT	CA_BIND 552 563
FT	CA_BIND 614 622
FT	SITE 1139 1142
FT	DISULFID 54 64
FT	DISULFID 660 669
FT	DISULFID 675 728
FT	DISULFID 780 786
FT	DISULFID 850 858
FT	DISULFID 1002 1044
FT	DISULFID 1047 1044
FT	CARBOHYD 46 46
FT	CARBOHYD 72 72
FT	CARBOHYD 77 77
FT	CARBOHYD 84 84
FT	CARBOHYD 189 189

[illegible]


```

or send an email to license@usb.sib.ch).
EMBL: X66748; CAA65510.1;
InterPro: IPR004018; GAF: 1;
InterPro: IPR004594; HATPase_c;
InterPro: IPR004599; HIS_KIN_sub;
InterPro: IPR004661; His_KinA;
InterPro: IPR001610; PAC;
InterPro: IPR000014; PAS;
InterPro: IPR001294; Phytochrome;
Pfam: PF01590; GAF; 1;
Pfam: PF02518; HATPase_c; 1;
Pfam: PF00989; PAS; 2;
Pfam: PF00360; phytochrome; 1;
Pfam: PF00512; signal; 1;
PRINTS: PR01033; PHYTOCHROME;
SMART: SM00065; GAF; 1;
SMART: SM00387; HATPase_c; 1;
SMART: SM00388; HIS_KIN; 1;
SMART: SM00086; PAC; 1;
SMART: SM00091; PAS; 2;
PROSITE: PS00109; HIS_KIN; 1;
PROSITE: PS00112; PAS; 2;
PROSITE: PS00245; PHYTOCHROME_1; 1;
PROSITE: PS00046; PHYTOCHROME_2; 1;
KW Transcription regulation; Phytochrome; Chromophore;
Repeat;
FT DOMAIN 621 692 PAS 1;
FT DOMAIN 795 826 PAS 2;
FT DOMAIN 903 1123 HISTIDINE KINASE;
FT BINDING 332 342 CHROMOPHORE (by similarity);
SQ SEQUENCE 1141 AA; 126254 MW; 064A208FA9042FB CRR64;

Query Match 96.83; Score 40; BB 1; Length 1141;
Best Local Similarity 83.38; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 0; Labels 0; Gaps 0;

QY 1 VAPRSP 6
ID 82 IORGR 87

RESULT 4
GSPN_PSEAE
ID GSPN_PSEAE STANDARD; PRT: 245 AA;
AC Q51575; Q4H2B4;
DI 16-OCT-2001 (Ref. 40, created)
DI 16-OCT-2001 (Ref. 40, last sequence update)
DI 16-OCT-2001 (Ref. 40, last annotation update)
DE General secretion pathway protein N (Xpp protein).
EN XCPP OR PA3104.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
OX NCBI_TaxID 287.
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN ATCC 15692 / PAOI;
RX MEDLINE 95020542; PubMed-7934933;
RA Arizm M., Bally M., Ball C., Tomaszewski J., Terebik B., Filipek A.,
Lazdinski A.;
R1 "Xpp-mediated protein secretion in Pseudomonas aeruginosa:
R1 identification of two additional genes and evidence for regulation of
R1 xcp gene expression."
R1 Mol. Microbiol. 10:441-443(1993).
RN 121
RP SEQUENCE FROM N.A.
RC STRAIN ATCC 15692 / PAS1;
RX MEDLINE 20437437; PubMed-10984043;
RA Silver C.E., Blum X.G.W., Urwin A., Wierzbicki P., Wharmby P.,
R1 Hickey M.T., Wierzbicki P., Wierzbicki W., Wierzbicki T., Liorson M.,
R1 Garbow P.L., Gully L., Tellechea F., Westbrook W.D., Yuan Y.,
R1 Rupp U., Guller S.R., Silver C.E., Lis A., Liorson M.,

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SA Saito K.A., Spector D.B., Ward G.K., Su W.Z., Paulsen O.,
RA Koller J., Saito M.H., Hancock R.E.W., Lory S., Olson M.V.;
R1 "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
R1 opportunistic pathogen."
R1 Nature 406:969-964(2000).
RN 131
RX SCS-3-11156; AccZ1104; Ado; Isobutyryl;
RX MEDLINE 96012575; PubMed-8769613;
RA Reeves S., Lazdinski A., Filipek A.;
R1 "Membrane topology of three Xcp proteins involved in xcp-protein
R1 transport by Pseudomonas aeruginosa."
R1 J. Bacteriol. 178:4297-4300(1996).
CV 1. FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (XPP) FOR THE
CV EXPORT OF PROTEINS. REQUIRED FOR THE TRANSLLOCATION OF A VARIETY
CV OF ENZYMES ACROSS THE OUTER MEMBRANE.
CV 1. SUBCELLULAR LOCATION: Type II membrane protein; Inner membrane.
CV
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CV
DR EMD: X66748; CAA65510.1;
DR EMD: AF041741; AAC06492.1;
KW Inner membrane; Transmembrane; Transport; Signal anchor;
KW Complete proteome;
FT DOMAIN 1 34 CYTOPLASMIC (POTENTIAL);
FT TRANSMEM 35 75 SIGNAL ANCHOR (TYPE II MEMBRANE PROTEIN)
(POTENTIAL);
FT DOMAIN 76 245 PERITRASMIC (POTENTIAL);
SQ SEQUENCE 245 AA; 25496 MW; DE972694D09A007 CRR64;

Query Match 90.43; Score 28; BB 1; Length 245;
Best Local Similarity 83.03; Pred. No. 0;
Matches 0; Conservative 1; Mismatches 0; Labels 0; Gaps 0;

QY 1 VAPRSP 6
ID 104 IORGR 104

EMBL 1
X66748; CAA65510.1;
DI 16-OCT-2001 STANDARD; PRT: 241 AA;
AC Q51575; Q4H2B4;
DI 16-OCT-1993 (Ref. 27, created)
DI 16-OCT-1993 (Ref. 41, last sequence update)
DI 16-OCT-2001 (Ref. 40, last annotation update)
DE XCPP protein.
EN XCPP OR PA3104.
OS Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
OX NCBI_TaxID 287.
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN ATCC 15692 / PAS1;
RX MEDLINE 94018699; PubMed-8412057;
RA Lazdinski A.,
R1 "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
R1 opportunistic pathogen."
R1 Nature 406:969-964(2000).
RN 121
RX SCS-3-11156; AccZ1104; Ado; Isobutyryl;
RX MEDLINE 96012575; PubMed-8769613;
RA Reeves S., Lazdinski A., Filipek A.;
R1 "Membrane topology of three Xcp proteins involved in xcp-protein
R1 transport by Pseudomonas aeruginosa."
R1 J. Bacteriol. 178:4297-4300(1996).
CV 1. FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (XPP) FOR THE
CV EXPORT OF PROTEINS. REQUIRED FOR THE TRANSLLOCATION OF A VARIETY
CV OF ENZYMES ACROSS THE OUTER MEMBRANE.
CV 1. SUBCELLULAR LOCATION: Type II membrane protein; Inner membrane.
CV
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CV
DR EMD: X66748; CAA65510.1;
DR EMD: AF041741; AAC06492.1;
KW Inner membrane; Transmembrane; Transport; Signal anchor;
KW Complete proteome;
FT DOMAIN 1 34 CYTOPLASMIC (POTENTIAL);
FT TRANSMEM 35 75 SIGNAL ANCHOR (TYPE II MEMBRANE PROTEIN)
(POTENTIAL);
FT DOMAIN 76 245 PERITRASMIC (POTENTIAL);
SQ SEQUENCE 245 AA; 25496 MW; DE972694D09A007 CRR64;

Query Match 90.43; Score 28; BB 1; Length 245;
Best Local Similarity 83.03; Pred. No. 0;
Matches 0; Conservative 1; Mismatches 0; Labels 0; Gaps 0;

QY 1 VAPRSP 6
ID 104 IORGR 104

```

RA Jenner D.J., Yang M., Ferrari E.,
RT "Localization of bacillus subtilis saccharyl) mutations to two linked
RT genes with signalling to the conserved presynaptic family of two
RT component signalling systems."
RL J. Bacteriol. 170:5102-5109(1988).
CC -1- SIMILARITY: TO S ADPINE PLASMIN DEF1 HYPOPHOSPHATE 15.6 E04 PROTEIN
CC (AC P13977) AND TO M.GENITALIUM M0256.
CC
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DR EMBL: Z18629; CAA79225.1;
DR EMBL: U56901; AAC44939.1;
DR EMBL: M23559; NCCT_ARE_TATHE_CDS.
DR EMBL: Z99122; CAPI5565.1;
DR PIR: D40191; D40191.
DR PIR: S28596; S28596.
DR Subtilisin; BG10394; deqV.
DR InterPro: IPR003797; D0F194.
DR Pfam: PF02645; D0F194; 1.
KW Complete proteome.
SQ Spolymorf 281 AA; 90.4% Score 28; DB 1; Length 281;
Query Match 90.4% Score 28; DB 1; Length 281;
Best Local Similarity 83.4% Pred. No. 67;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VORGER 6
DB 167 LQBSGR 172
ID VP6_HTV11 STANDARD; PRT: 425 AA.
AC P42934;
DT 01-OCT-1993 (rel. 27, Created)
DI 01-OCT-1993 (rel. 27, Last sequence update)
DT 15-DEC-1998 (rel. 37, Last annotation update)
DE VP6 protein (Minor inner core protein VP6).
GN S9.
OS Bluetongue virus (serotype 1) / isolate USA).
OC Viruses: dsRNA viruses: Reoviridae; orbivirus.
OX NCBI_TaxID: 33716;
RN [1]
PP MEDLINE: 93033709; PubMed: 1429371;
RA Hwang G.-Y., Chion J.-F., Yang Y.-Y., Li J.-K.-K.;
RT "Comparative sequence analyses of the conserved structural protein VP6
RT genes of five US bluetongue viruses."
RL Virus Res. 24:315-323(1992).
CC -1- FUNCTION: SUBPODS AND INTERACTS WITH THE GENOMIC DS RNA.
CC POSSESSES SS- AND DS-RNA-BINDING CAPACITY. ITS HYDROPHILIC
CC NATURE AND CAPABILITY TO BIND SS- AND DS RNA SUGGEST ITS
CC INTERACTIONS WITH BTV GENOMIC RNA.
CC -1- SUBCELLULAR LOCATION: INNER CAPSID.
CC -1- SIMILARITY: BELONGS TO THE REOVIRUSES VP6 FAMILY.
CC
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DR EMBL: L08670; AAA42819.1;
DR PIR: A48561; A48561.

DR InterPro: IPR001399; orbi_VP6.
DR Pfam: PF01516; orbi_VP6; 1.
DR PRINTS: PR09902; VP6AFSID.
KW Core protein.
FT DOMAIN 84 125 GLY RICH.
SQ SEQUENCE: 425 AA; 95.87% MW; 111960256740629 CRR04;
Query Match 90.4% Score 28; DB 1; Length 425;
Best Local Similarity 83.4% Pred. No. 67;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VORGER 6
DB 199 VERGER 204
ID VP6_HTV17 STANDARD; PRT: 425 AA.
AC P42935;
DT 01-OCT-1993 (rel. 27, Created)
DI 01-OCT-1993 (rel. 27, Last sequence update)
DE VP6 protein (Minor inner core protein VP6).
GN S9.
OS Bluetongue virus (serotype 1) / isolate USA).
OC Viruses: dsRNA viruses: Reoviridae; orbivirus.
OX NCBI_TaxID: 33717;
RN [1]
PP MEDLINE: 93033709; PubMed: 1429371;
RA Hwang G.-Y., Chion J.-F., Yang Y.-Y., Li J.-K.-K.;
RT "Comparative sequence analyses of the conserved structural protein VP6
RT genes of five US bluetongue viruses."
RL Virus Res. 24:315-323(1992).
CC -1- FUNCTION: SUBPODS AND INTERACTS WITH THE GENOMIC DS RNA.
CC POSSESSES SS- AND DS RNA-BINDING CAPACITY. ITS HYDROPHILIC
CC NATURE AND CAPABILITY TO BIND SS- AND DS RNA SUGGEST ITS
CC INTERACTIONS WITH BTV GENOMIC RNA.
CC -1- SUBCELLULAR LOCATION: INNER CAPSID.
CC -1- SIMILARITY: BELONGS TO THE REOVIRUSES VP6 FAMILY.
CC
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DR EMBL: L08671; AAA42820.1;
DR InterPro: IPR001399; orbi_VP6.
DR Pfam: PF01516; orbi_VP6; 1.
DR PRINTS: PR09902; VP6AFSID.
KW Core protein.
FT DOMAIN 84 125 GLY RICH.
SQ SEQUENCE: 425 AA; 95.87% MW; 108408712732A34 CRR04;
Query Match 90.4% Score 28; DB 1; Length 425;
Best Local Similarity 83.4% Pred. No. 67;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VORGER 6
DB 199 VERGER 204
ID VP6_HTV17 STANDARD; PRT: 425 AA.
AC P42935;
DT 01-OCT-1993 (rel. 27, Created)
DI 01-OCT-1993 (rel. 27, Last sequence update)
DE VP6 protein (Minor inner core protein VP6).
GN S9.
OS Bluetongue virus (serotype 1) / isolate USA).
OC Viruses: dsRNA viruses: Reoviridae; orbivirus.
OX NCBI_TaxID: 33717;
RN [1]
PP MEDLINE: 93033709; PubMed: 1429371;
RA Hwang G.-Y., Chion J.-F., Yang Y.-Y., Li J.-K.-K.;
RT "Comparative sequence analyses of the conserved structural protein VP6
RT genes of five US bluetongue viruses."
RL Virus Res. 24:315-323(1992).
CC -1- FUNCTION: SUBPODS AND INTERACTS WITH THE GENOMIC DS RNA.
CC POSSESSES SS- AND DS RNA-BINDING CAPACITY. ITS HYDROPHILIC
CC NATURE AND CAPABILITY TO BIND SS- AND DS RNA SUGGEST ITS
CC INTERACTIONS WITH BTV GENOMIC RNA.
CC -1- SUBCELLULAR LOCATION: INNER CAPSID.
CC -1- SIMILARITY: BELONGS TO THE REOVIRUSES VP6 FAMILY.
CC
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DR EMBL: L08670; AAA42819.1;
DR PIR: A48561; A48561.

DT 15-DEC-1998 (rel. 37, last annotation update)
 DE VP6 protein (Minor inner core protein VP6).
 GN S9.
 OS Bluetongue virus (serotype 17/2 last sequence update)
 OC Viruses: dsRNA viruses, Reoviridae, Orbivirinae.
 OX NCBI TaxID: 42718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 96064709; PubMed 1429471;
 RA Iwano G. Y., Choud J. F., and Y. Y., Li J.K., K.;
 RT "Comparative sequence analysis of the genome structural protein VP6
 genes of five reovirus-like viruses."
 RL Virus Res. 24:315-323(1992).
 CC -F- FUNCTION: SUBUNITES AND INTERACTS WITH THE GIN-40R LG RNA.
 CC POSSESSES SS- AND DS-RNA BINDING CAPACITY. ITS HYDROPHILIC
 CC NATURE AND CAPABILITY TO BIND SS- AND DS-RNA SUGGESTS ITS
 CC INTERACTIONS WITH BTV GENOMIC RNA.
 CC -F- SUBCELLULAR LOCATION: INNER CAPSID.
 CC -F- SIMILARITY: BELONGS TO THE REOVIRUSES VP6 FAMILY.
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 DR EMBL: L08672; AAA2821.1; -;
 DR InterPro: IPR001499; orbi_VP6.
 DR Pfam: PF01516; orbi_VP6; 1.
 DR PRINTS: PR00902; VP6CAPSID.
 KW Core protein.
 FT DOMAIN 84 125 GLY RICH.
 SQ SEQUENCE 425 AA: 45317 MW: 46059642.62 kDa 0.664;
 1 VQVGR 6
 11111
 199 VERGR 204

Query Match
 Best Local Similarity 90.4%; Score 28; DB 1; Length 425;
 Matches 5; Conservatve 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQVGR 6
 11111
 DQ 199 VERGR 204
 RESULT 9
 VP61_RTV10 STANDARD; PRI: 42% AA.
 AC I23066;
 DT 01-NOV-1991 (rel. 20, created)
 DI 01-FEB-1996 (rel. 35, last sequence update)
 DI 15-DEC-1998 (rel. 37, last annotation update)
 DE VP6 protein (Minor inner core protein VP6) (Version 1).
 GN S9.
 OS Bluetongue virus (serotype 17/2 last sequence update)
 OC Viruses: dsRNA viruses, Reoviridae, Orbivirinae.
 OX NCBI TaxID: 19406;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 89290576; PubMed 2544660;
 RA Kakisho A., Yu Y., Yamaguchi S., Roy P.;
 RT "Completed of the sequence of bluetongue virus serotype 10 by the
 RT characterization of a structural protein, VP6, and a non structural
 RT protein, NS2."
 RL J. Gen. Virol. 70:1677-1689(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 90445726; PubMed 2166649;
 RA Roy P., Marshall J.J.A., French L.J.;
 RT "Structure of the bluetongue virus genome and its encoded proteins."
 RL Curr. Top. Microbiol. Immunol. 162:43-87(1991).
 RN [3]
 RP REVISIONS.

RA Bluetongue virus.
 CC Submitted (2002-09-09) to the EMBL/GenBank/Tran databases.
 CC -F- FUNCTION: SUBUNITES AND INTERACTS WITH THE GIN-40R LG RNA.
 CC POSSESSES SS- AND DS-RNA BINDING CAPACITY. ITS HYDROPHILIC
 CC NATURE AND CAPABILITY TO BIND SS- AND DS-RNA SUGGESTS ITS
 CC INTERACTIONS WITH BTV GENOMIC RNA.
 CC -F- SUBCELLULAR LOCATION: INNER CAPSID.
 CC -F- SIMILARITY: BELONGS TO THE REOVIRUSES VP6 FAMILY.
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 DR EMBL: L08672; AAA00499.1;
 DR Pfam: PF01516; orbi_VP6.
 DR InterPro: IPR001499; orbi_VP6.
 DR Pfam: PF01516; orbi_VP6; 1.
 DR PRINTS: PR00902; VP6CAPSID.
 KW Core protein.
 FT DOMAIN 84 125 GLY RICH.
 SQ SEQUENCE 425 AA: 45315 MW: 50049644.07 kDa 0.664;
 1 VQVGR 6
 11111
 204 VERGR 204
 Query Match
 Best Local Similarity 88.4%; Score 28; DB 1; Length 429;
 Matches 5; Conservatve 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQVGR 6
 11111
 DQ 204 VERGR 204
 RESULT 10
 K11H_BSV24 STANDARD; PRI: 47% AA.
 ID K11H_BSV24
 AC P04407;
 DT 13-APR-1987 (rel. 05, created)
 DI 15-DEC-1998 (rel. 37, last sequence update)
 DI 30-MAY-2000 (rel. 39, last annotation update)
 DE Thymidine kinase (P04407.1.21)
 GN TK
 OS Herpes simplex virus (type 2 / strain xxx)
 OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
 OX Alphaherpesvirinae; Simplexvirus.
 OX NCBI TaxID: 10413;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 84080454; PubMed 6417005;
 RA Kit S., Kit M., Quast H., Trkola D., Otsuki H.;
 RT "Thymidine kinase gene and predicted amino acid sequence of thymidine
 RT kinase polypeptide and its comparison with the HSV-1 thymidine kinase
 RT gene."
 RL J. Virol. 61:1568-1570(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 84216400; PubMed 6404366;
 RA Smith M.A., Gallooly D.A.;
 RT "Nucleotide sequence of the herpes simplex virus type 2 thymidine
 RT kinase gene."
 RL J. Virol. 49:1045-1050(1983).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 86142700; PubMed 2829709;
 RA Kit S., Otsuki H., Trkola D., Otsuki H., Trkola D., Otsuki H.;
 RT "Nucleotide sequence changes in thymidine kinase gene of herpes
 RT simplex virus type 2 clones from an isolate of a patient treated with

RT acyclovir.";
 RL Antimicrob. Agents Chemother. 31:1483-1490(1987).
 RC -1: CATALYTIC ACTIVITY: ATP + thymidine + ADP + thymidine 5'-
 CC phosphate.
 CC -1: SIMILARITY: BELONGS TO THE HYDROXYMETHYL-TRANSFERASE FAMILY.
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 CC
 CC EMBL: X01712; CAA35868.1;
 CC F001: V00466; CAA32940.1;
 CC EMBL: M29942; AAA45856.1;
 CC PIR: A06613; KIBET3.
 CC HSP: P03176; 2VTK.
 CC InterPro: IPR001496; 19.1.1.1
 CC Pfam: PF00693; TK_herpes_1.
 CC Transferr: P001519; TK_herpes_1.
 CC KW Transferrase; Kinase; DNA synthesis; ATP binding.
 CC FT NP_BIND 56 63 ATP (PROBABLE).
 CC FT DOMAIN 168 176 NUCLEOTIDE-BINDING (POTENTIAL).
 CC FT CONFLICT 271 271 MISSING (IN PDB 1).
 CC SQ SEQUENCE 376 AA; 40467 MW; 981048B0B8A38A5_GcG64,
 Query Match 90.3%; Score 28; DB 1; Length 376,
 Best Local Similarity 83.3%; Pred. NO. 77;
 Matches 5; Conservation 1; Mismatches 0; Gaps 0;
 QY 1 VORGR 6
 DB 250 LQGR 255
 RESULT 11
 PHN1_DRS1
 ID PHN1_DRS1 STANDARD; PRT; 550 AA;
 AC P12944;
 DI 01-JAN-1990 (Rel. 13, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DI 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Periplasmic [NifH] hydrogenase large subunit precursor (pI 1.18, 99.1)
 DE (NifH hydrogenase large chain).
 DE HYDB.
 CC Desulfotribio citus.
 CC Bacteria: Proteobacteria; delta subdivision; Desulfotribio.
 CC NCBI_TaxID=879;
 LI 11
 RN SEQUENCE FROM N.A. AND REVISIONS.
 RP Desulfotribio citus; PubMed 811029;
 RX MEDLINE 811029; PubMed 8122743;
 RA Li C., Peck H.D., Jr., Le Gall J., Przytyla A.E.;
 RT "Cloning, characterization, and sequencing of the genes encoding the
 RT large and small subunits of the periplasmic [NifH]hydrogenase of
 RT Desulfotribio citus.";
 RT Desulfotribio citus.
 RL DNA 6:549-551(1987).
 RN [2]
 RP SEQUENCE FROM N.A. AND REVISIONS.
 PX Desulfotribio citus; PubMed 811029;
 PA Voordouw G., Meent N.K., Le Gall J., Choi E.S., Peck H.D., Jr.,
 RA Przytyla A.E.;
 RT "Analysis and comparison of nucleotide sequences encoding the genes
 RT for [NifH] and [NifHse] hydrogenases from Desulfotribio citus and
 RT Desulfotribio bacularius.";
 RL J. Bacteriol. 171:2804-2809(1989).
 RN [3]
 RP SEQUENCE OF 1-29.
 RX MEDLINE 88106446; PubMed 8222275;
 RA Prigent-Bisot B., Ho S.H., Li C., Meent N., Choi E.S., Przytyla A.E.,
 PA Prigent-Bisot B., Peck H.D., Jr., Peck H.D., Le Gall J., Le Gall B.,
 RA Moore L., Moore J.J.C., Pail D., Rayn B.H.;

"Identification of three classes of hydrogenase in the genus
 RL Desulfotribio.";
 RC Biochem. Biophys. Res. Commun. 149:369-377(1987).
 CC [4]
 CC X-RAY CRYSTALLOGRAPHY (2.0 Å RESOLUTION).
 CC MEDLINE 95157429; PubMed 7864413;
 CC Volbeda A., Charon M.-H., Piras G., Hatchikian E.C., Frey M.,
 CC Fontecilla-Camps J.C.;
 CC "Crystal structure of the nickel-iron hydrogenase from Desulfotribio
 CC citus.";
 CC Nature 373:580-587(1995).
 CC X-RAY CRYSTALLOGRAPHY (2.0 Å RESOLUTION).
 CC TETRAEDOXIN + H₂.
 CC -1: COFACTOR: ONE NICKEL ION, TWO 4FE 4S CLUSTERS AND ONE 3FE 4S
 CC CLUSTER. THE LARGE SUBUNIT IS HIGHLY IDENTICAL TO THE NICKEL ION.
 CC -1: SUBCELLULAR LOCATION: PERIPLASMIC.
 CC -1: MISCELLANEOUS: TERRAPS THE LEADER OF THE SMALL SUBUNIT SERVES AS A
 CC TRANSPORT VEHICLE FOR BOTH SUBUNITS.
 CC -1: SIMILARITY: BELONGS TO THE [NifH]/[NifHse] H2E HYDROGENASE
 CC SUBUNIT FAMILY.
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 CC
 CC EMBL: M19993; AAA22478.1; ALT_SEQ.
 CC PIR: B42345; HQHWDG.
 CC PIR: D27480; D27480.
 CC PIR: JEVV; G8 NOV-96.
 CC InterPro: IPR001501; NifHse_Hases.
 CC Pfam: PF00374; NifHse_Hases; 1.
 CC PROSITE: PS00507; NIF_HENASE_L1; 1.
 CC PROSITE: PS00508; NIF_HENASE_L2; 1.
 CC KW oxidoreductase; periplasmic; Nickel; 3D structure.
 CC INI1_MET 0 0
 CC CHAIN 1 535 PERIPLASMIC [NifH] HYDROGENASE LARGE
 CC SUBUNIT.
 CC PROPEP 546 550
 CC METAL 64 64 NICKEL.
 CC METAL 67 67 NICKEL.
 CC METAL 629 629 NICKEL.
 CC METAL 542 542 NICKEL.
 CC SEQUENCE 550 AA; 61449 MW; 1FCE6AFA7519840_GcG64;
 Query Match 90.3%; Score 28; DB 1; Length 550;
 Best Local Similarity 83.3%; Pred. NO. 11002;
 Matches 1; Conservation 1; Mismatches 0; Gaps 0;
 QY 1 VORGR 6
 DB 470 VORGR 475
 RESULT 12
 ENV_SIVM1
 ID ENV_SIVM1; CAA35868.1;
 AC P05885; CAA35868.1; CAA35868.1;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DI 01-NOV-1988 (Rel. 09, Last annotation update)
 DI 15-JUL-1999 (Rel. 37, Last annotation update)
 DE Desulfotribio citus; PubMed 811029;
 DE Desulfotribio citus; PubMed 811029;
 GN ENV.
 CC Simian immunodeficiency virus (MML42-83 isolate) (SIV-MAC).
 CC Viruses: Retroviridae; Retroviridae; Lentiviridae.
 CC NCBI_TaxID=11733;
 RN [1]
 RP SEQUENCE FROM N.A.

KW Ribosomal protein.
 FI NON_TER 1
 SE SEQUENCE 153 AA, 17999 MW, AA0177101415:AAA6 (P0664)
 Query Match 87.1%; Score 27; DB 1; Length 153;
 Best local similarity 83.48; Pred. No. 55;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VRRGR 6
 I: I I I I
 DB 15 VRRGR 20

RESULT 15

FRTH_RABIT STANDARD; PRI: 164 AA.
 AC P25915;
 01-MAY-1992 (Rel. 22; Created)
 01-MAY-1992 (Rel. 22; Last sequence update)
 15-JUL-1999 (Rel. 38; Last annotation update)
 DE Ferritin heavy chain (Ferritin H subunit) (Fragment).
 GN FTH.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID:9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE:Vascular smooth muscle;
 RX MEDLINE:92011647; PubMed:1655764;
 RA Lian G., Chan L.M., Feng P.;
 RT "Increased ferritin gene expression is both promoted by cAMP and a
 marker of growth arrest in rabbit vascular smooth muscle cells."
 RL J. Biol. Chem. 266:18819-18826(1991).
 CC -!- FUNCTION: FERRITIN IS AN INTRACELLULAR MOLECULE THAT STORES IRON
 IN A SOLUBLE, NONTOXIC, READILY AVAILABLE FORM. THE FUNCTIONAL
 MOLECULE, WHICH IS COMPOSED OF 24 CHAINS, IS ROUGHLY SPHERICAL
 AND CONTAINS A CENTRAL CAVITY IN WHICH THE POLYMERIC FERRIC IRON
 CORE IS DEPOSITED.
 CC -!- MISCELLANEOUS: THERE ARE TWO TYPES OF FERRITIN SUBUNITS: L (LIGHT)
 CHAIN AND H (HEAVY) CHAIN. THE MAJOR CHAIN CAN BE LIGHT OR HEAVY,
 DEPENDING ON THE SPECIES AND TISSUE TYPE.
 CC -!- SIMILARITY: BELONGS TO THE FERRITIN FAMILY.
 CC -----
 CC This SWISS-Prot entry is copyright. It is produced through a collaborat
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities is hereby strictly prohibited (S. Holtkamp and all others who
 or send an email to licens@isb.sib.ch).
 CC -----
 CC EMBL: M63912; AAA31247.1;
 DR HSSP: P02794; 2PHA.
 DR InterPro: IPR001519; Ferritin.
 DR Pfam: PF00210; ferritin_1.
 DR ProDom: PD000971; Ferritin_1.
 DR PROSITE: PS00540; FERRITIN_1;
 DR PROSITE: PS00204; FERRITIN_2;
 KW Iron storage; Multigene family.
 FT NON_TER 1
 I: I
 FT METAL 9 9 IRON (BY SIMILARITY).
 FT METAL 40 40 IRON (BY SIMILARITY).
 FT METAL 43 43 IRON (BY SIMILARITY).
 FT METAL 44 44 IRON (BY SIMILARITY).
 FT METAL 46 46 IRON (BY SIMILARITY).
 FT METAL 47 47 IRON (BY SIMILARITY).
 FT METAL 89 89 IRON (BY SIMILARITY).
 FT METAL 124 124 IRON (BY SIMILARITY).
 FT METAL 124 124 IRON (BY SIMILARITY).
 SQ SEQUENCE 164 AA; 19192 MW; 6180505CFRFRH389 (P0664);
 Query Match 87.1%; Score 27; DB 1; Length 164;
 Best Local Similarity 100.0%; Pred. No. 59;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VRRGR 6
 I: I I I I
 DB 57 VRRGR 61
 Search completed: October 22, 2002, 16:00:35
 Job time: 1:50894 secs

Copyright © 1993 by Verso

1M protein - protein search, using sw model

run on: October 22, 2002, 16:00:02 ; Search time: 1,6393 Seconds
(without all elements)
635,260 Milliseconds total (0.635260 seconds)

Title: 8-847-966, 6.0-38-8
US-09, 996-738-8

For the Survey: 41

Sequence: 1 VORGEH 6

1001-1005

Figure 10.10: $\text{capex}(0.5)$ (X-axis) and $\text{capex}(1.0)$ (Y-axis)

Source: *ibid.*, 1799490, 1799491, 1799492.

total number of bits satisfying chosen parameters:

Journal of Management Inquiry 18(4) 405-421

[illegible]

Post-Processing: Minimum Match: 0%

Maximum

First published in 1998
First published in 1998

```

Database :
SPTREMBL_19: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_orchidellae: *
9: sp_phages: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_meclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archaeap: *

```

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	SUMMARIES			ID	Description
	Score	Query Match	Length		
1	31	100.0	96	15	091897 human immun
2	22	100.0	114	2	047482 escherichia
3	41	100.0	278	2	007497 mycobacteri
4	41	100.0	394	2	044416 arabidorti
5	41	100.0	424	16	098806 rhizobium l
6	30	96.8	130	1	091006 sulfolobus
7	40	96.8	269	1	074066 venteribacum
8	40	96.8	273	1	074043 venteribacum
9	40	96.8	273	2	094080 streptomyce
10	28	90.3	72	2	094080 streptomyce
11	28	90.3	144	17	026540 methanocor
12	28	90.3	141	4	094080 streptomyce
13	29	90.3	212	10	094194 pseudomonas
14	28	90.3	245	15	091312 pseudomonas
15	29	90.3	293	16	092789 pseudomonas
16	28	90.3	299	3	090135 pseudomonas

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DT 01-DEC-2001 (TRENBERG, 19, Last annotation update)
DE ORF114.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
CX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:90170953; PubMed=2155230;
EA Chen C.-M., Ye Q.-Z., Zhu Z., Warner B.H., Walsh E.L.,
FT "Klebsiella" biology of carbon-phosphorus bond cleavage, cloning and
RT sequencing of the pbn (psbD) genes involved in alkylphosphonate uptake
RT and C-P lyase activity in Escherichia coli B.
RL J. Biol. Chem. 265:4461-4471(1990)
DR EMBL: J05260; AAC24511.1; -.
SQ SEQUENCE 114 AA; 12496 MW; F754EC426153011A GR064;

Query Match 100.0%; Score 31; DB 2; Length 114;
Best local similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGR 6
DB 40 VORGR 45

RESULT 4
Q07497
ID 007497 PRELIMINARY; PRT; 278 AA.
AC 007497;
DT 01-JUL-1997 (TRENBERG, 04, Created)
DT 01-JUL-1997 (TRENBERG, 04, Last sequence update)
DT 01-DEC-2001 (TRENBERG, 19, Last annotation update)
DE MAV278.
GN MAV278.
OS Mycobacterium avium.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
CX NCBI_TaxID=1764.
RN [1]
RP SEQUENCE FROM N.A.
RX SIPATH C1F10.
RX MEDLINE:98195739; PubMed=95334249;
EA Labo M., Gastert L., Rossi E.D., Speziale P., Rivardi G.,
FT "determination of a 1543 bp nucleotide sequence around the hsaA gene
RT of Mycobacterium avium and similarity analysis of the products of
RT putative ORFs."
RL Microbiology 144:807-814(1998).
DR EMBL: AF902133; AAC42311.1; -.
SQ SEQUENCE 278 AA; 30646 MW; AE95A67F0D0097 GR064;

Query Match 100.0%; Score 31; DB 2; Length 278;
Best local similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGR 6
DB 164 VORGR 169

RESULT 4
Q44416
ID Q44416 PRELIMINARY; PRT; 394 AA.
AC Q44416;
DT 01-NOV-1996 (TRENBERG, 01, Created)
DT 01-NOV-1996 (TRENBERG, 01, Last sequence update)
DT 01-DEC-2001 (TRENBERG, 19, Last annotation update)
DE ENDOGLUCANASE.
GN CHLC.
OS Aerobacterium tumefaciens.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
CX NCBI_TaxID=358;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:95164506; PubMed 7860585;
EA Matthysse A.G., White S., Lightfoot P.J.
FT "Genes required for cellulose synthesis in Aerobacterium
RT tumefaciens."
RL J. Bacteriol. 177:1059-1075(1995).
DR EMBL: L38609; AAC14331.1; -.
DR INTERPRO: IPR02037; Glyco_hydro_8.
DR Pfam: PF01275; Glyco_hydro_8; 1.
SQ SEQUENCE 334 AA; 42358 MW; B9C0755CEB333E GR064;

Query Match 100.0%; Score 31; DB 2; Length 394;
Best local similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGR 6
DB 262 VORGR 267

RESULT 5
Q98B06
ID Q98B06 PRELIMINARY; PRT; 424 AA.
AC Q98B06;
DT 01-OCT-2001 (TRENBERG, 18, Created)
DT 01-OCT-2001 (TRENBERG, 18, Last sequence update)
DT 01-OCT-2001 (TRENBERG, 18, Last annotation update)
DE M415421.
GN M415421.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Mesorhizobium.
CX NCBI_TaxID 381;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN:MAPP30009;
RX MEDLINE:21282909; PubMed 11214968;
EA Kambo J., Nakamura Y., Sato S., Asamiya H., Kato T., Sasamoto S.,
EA Katsuda A., Ikesawa K., Ishikawa A., Kawashima K., Kimura T.,
EA Kishida Y., Miyokawa G., Kohara M., Matsuno M., Matsuno A.,
EA Nishizaki Y., Nakayama S., Nakazaki S., Shimizu S., Shimizu M.,
EA Takouchi G., Yamada M., Tabata S.,
FT "Complete genome structure of the nitrogen fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DR EMBL: AP004006; BAB1876.1; -.
KW Transferrase; complete proteome.
SQ SEQUENCE 424 AA; 46939 MW; 921155E265241F1B GR064;

Query Match 100.0%; Score 31; DB 16; Length 424;
Best local similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGR 6
DB 60 VORGR 65

RESULT 6
Q9UW06
ID Q9UW06 PRELIMINARY; PRT; 140 AA.
AC Q9UW06;
DT 01-MAY 2000 (TRENBERG, 13, Created)
DT 01-MAY 2000 (TRENBERG, 13, Last sequence update)
DT 01-MAY 2000 (TRENBERG, 13, Last annotation update)
DE HYPOPHOSPHATASE, 14.0 KDA PROTEIN.
GN CRF_022_010.
OS Sulfotobius solitarius.
OC Archaea; Crenarchaeota; Sulfotobiales; Sulfotobaceae; Sulfotobios.
CX NCBI_TaxID 2387;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-DSM 16117 / P2;
RA Charlebois R.L., Singh R.K., Chan-Waiher C.C., Y., Allard G., Chow C.,
RA Cantalieri F., Curtis R., Duquet M., Eraso G., Fardy D.,
RA Gausterer T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C.,
RA Kuswaha N., Laffour E., Medina N., Penn X., Penny S.L., Shae G.,
PA St. Jean A., Van Der Grest J., Young F., Zengovic Y., Zocchetti W.F.,
RA Radon M.A., Sensen C.W.;
RT "Gene content and organization of a 281-kbp contig from the genome of
RT the extremely thermophilic archaeon, Sulfolobus solfataricus P2."
RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y18940; CAC57758.1; -.
KW Hypothetical protein.
SQ
SEQUENCE 130 AA; 14047 MW; 94B19DA20F333197 CRC64;

Query Match
Best Local Similarity 96.8%; Score 30; DB 1; Length 130;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGER 6
DB 109 LQ6GR 60
|||||

RESULT 7
QY4066
ID 074066 PRELIMINARY; PRI: 27% AA;
AC 074066;
DT 01-NOV-1998 (EMBLrel. 08, Created)
DI 01-NOV-1998 (EMBLrel. 08, Last sequence update)
DI 01-JUN-2001 (EMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 30.7 KDA PROTEIN.
OS Cenarchaeum symbiosum.
OC Archaea; Crenarchaeota; Cenarchaeum.
OX NCBI_TaxID 46770;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN A;
RA Schlieper C., Deland E.F., Preston C.M., Feldman R.A., Wu K.Y.,
RA Swanson R.V.;
RT "Genomic analysis reveals chromosomal variation in natural populations
RT of the uncultured psychrophilic archaeon Cenarchaeum symbiosum."
RC EMBL: AF083072; AAC562709.1; -.
DR InterPro: IPR004115; ParBc.
DR Pfam: PF02195; ParBc.1.
DR SMART: SM00470; ParBc.1.
KW Hypothetical protein.
SQ
SEQUENCE 269 AA; 30689 MW; AA452167AB160458 CRC64;

Query Match
Best Local Similarity 96.8%; Score 30; DB 1; Length 269;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGER 6
DB 55 LQ6GR 60
|||||

RESULT 8
QY4043
ID 074043 PRELIMINARY; PRI: 27% AA;
AC 074043;
DT 01-NOV-1998 (EMBLrel. 08, Created)
DI 01-NOV-1998 (EMBLrel. 08, Last sequence update)
DI 01-JUN-2001 (EMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 31.1 KDA PROTEIN.
OS Cenarchaeum symbiosum.
OC Archaea; Crenarchaeota; Cenarchaeum.
OX NCBI_TaxID: 46770;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN A;

```

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PX MEDLINE 9744440; PubMed 9744440;
RA Schlieper C., Deland E.F., Preston C.M., Feldman R.A., Wu K.Y.,
RA Swanson R.V.;
RT "Genomic analysis reveals chromosomal variation in natural populations
RT of the uncultured psychrophilic archaeon Cenarchaeum symbiosum."
RC EMBL: AF083072; AAC562686.1; -.
DR InterPro: IPR004115; ParBc.
DR Pfam: PF02195; ParBc.1.
DR SMART: SM00470; ParBc.1.
KW Hypothetical protein.
SQ
SEQUENCE 273 AA; 31103 MW; 6840684F180F619E CRC64;

Query Match
Best Local Similarity 96.8%; Score 30; DB 1; Length 273;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGER 6
DB 59 LQ6GR 64
|||||

RESULT 9
QY4040
ID 074040 PRELIMINARY; PRI: 27% AA;
AC 074040;
DT 01-JUN-2001 (EMBLrel. 17, Created)
DI 01-JUN-2001 (EMBLrel. 17, Last sequence update)
DI 01-OCT-2001 (EMBLrel. 18, Last annotation update)
DE HYPOTHETICAL 29.5 KDA PROTEIN.
OX NCBI_TaxID: 46770;
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteriae; Streptomyces.
OC Actinomycetales; Streptomyces; Streptomyces.
OX NCBI_TaxID 1902;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN A3(2);
RA Schlieper C., Deland E.F., Harris D.,
RA Swanson R.V., Harris D.;
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN 121
RP SEQUENCE FROM N.A.
RC STRAIN A3(2);
RA Cordano A.M., Parkhill J., Barrett J., Rajandream M.A.;
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN 131
RP SEQUENCE FROM N.A.
RC STRAIN A3(2);
RA Medline 9700055; PubMed 9843405;
RA Rodenbach M., Krieser H.M., Benayahu D., Eichner A., Gellum J.,
RA Kinoshita H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 9-Mb Streptomyces coelicolor A3(2) chromosome."
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL: AL034945; CAC42681.1; -.
DR InterPro: IPR000182; GAF.
DR Pfam: PF01590; GAF.1.
DR SMART: SM00465; GAF.1.
KW Hypothetical protein.
SQ
SEQUENCE 274 AA; 29523 MW; 5959A6440490679 CRC64;

Query Match
Best Local Similarity 96.8%; Score 30; DB 2; Length 274;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGER 6
DB 61 LQ6GR 66
|||||

RESULT 10
QY4039
ID 074039 PRELIMINARY; PRI: 27% AA;

```

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AC Q93807;
DI 01-DEC-2001 (TrEMBLrel. 19, Created)
DI 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
DE FERREDOXIN.
OS Streptomyces lavendulae.
OC Bacteria; Firmicutes; Actinobacteriia; Actinobacteriales.
OC Actinomycetales; Streptomyces; Streptomyces; Streptomyces.
OX NCBI_TaxID:1914;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354012; PubMed 11447274;
RA Chiu H.T., Hubbard B.K., Shah A.N., Fiske J., Frodenberg K.A.,
RA Walsh C.T., Khosla C.;
RT "Molecular cloning and sequence analysis of the complexatin
RT biosynthetic gene cluster of Streptomyces lavendulae."
RL Proc. Natl. Acad. Sci. U.S.A. 98:8508-8554(2001).
RL EMBL: AF496507; AAK91433.1;
SEQUENCE 72 AA; 7842 MW; 6C29B9C12F99B156 CR664;

Query Match          90.3%; Score 28; DB 2; Length 72;
Best Local Similarity 83.3%; Pred. No. 1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGGK 6
   1:|||||
DB 66 VERGR 71

RESULT 11
Q26530
ID Q26530 PRELIMINARY; PRT; 134 AA.
AC Q26530;
DI 01-JAN-1998 (TrEMBLrel. 05, Created)
DI 01-JAN-1998 (TrEMBLrel. 05, last sequence update)
DI 01-OCT-2001 (TrEMBLrel. 18, last annotation update)
DE HYPOTHETICAL 14.7 KDA PROTEIN.
GN MTH430.
OS Methanothermobacter thermoautotrophicus.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales.
OC Methanothermobacter.
OX NCBI_TaxID:115262;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98037514; PubMed 9373463;
RA Smith D.B., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Roberts T.,
RA Aldredge T., Bashford-Dubch S., Blakey M., Cook F., Gilbert K.,
RA Harrison D., Hoang L., Keegan P., Lamm W., Parker R., Qiu F.,
RA Spadafora F., Viscardi R., Wang Y., Wroblewski J., Gibson K.,
RA Jiwani N., Caruso A., Bush D., Sater R., Patwell D., Prabhakar S.,
RA McDougall S., Shiner G., Goyal A., Pietrowski S., Charch C.M.,
RA Daniels G.J., Mao J., Rice P., Halliwell J., Reese J.M.;
RT "Complete genome sequence of Methanothermobacter thermoautotrophicum
RT deltaH: functional analysis and comparative genomics."
PI J. Bacteriol. 194:3631-3641(2002)
FW EMBL: AF000827; AAB84936.1;
FW F2P 152111.1; 16372 MW; 5P32AP4C16457928 CR674;
SEQUENCE 144 AA; 14672 MW; 5P32AP4C16457928 CR674;

Query Match          90.3%; Score 28; DB 17; Length 144;
Best Local Similarity 83.3%; Pred. No. 1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGGK 6
   1:|||||
DB 108 LQGGK 113

RESULT 12
Q9BX98
ID Q9BX98 PRELIMINARY; PRT; 141 AA.
AC Q9BX98;

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DI 01-JUN-2001 (TrEMBLrel. 17, Created)
DI 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
DE UB1QUITIN A-52 NUCLEOLAR PROTEIN P23788 PRODOT 1
DE (FRAGMENT).
GN BBA52.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Trachata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354012; PubMed 11447274;
RA Chiu H.T., Hubbard B.K., Shah A.N., Fiske J., Frodenberg K.A.,
RA Walsh C.T., Khosla C.;
RT "Molecular cloning and sequence analysis of the complexatin
RT biosynthetic gene cluster of Streptomyces lavendulae."
RL Proc. Natl. Acad. Sci. U.S.A. 98:8508-8554(2001).
RL EMBL: AF496507; AAK91433.1;
SEQUENCE 72 AA; 7842 MW; 6C29B9C12F99B156 CR664;

Query Match          90.3%; Score 28; DB 4; Length 141;
Best Local Similarity 83.3%; Pred. No. 1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGGK 6
   1:|||||
DB 4 LQGGK 9

RESULT 13
Q94IK9
ID Q94IK9 PRELIMINARY; PRT; 212 AA.
AC Q94IK9;
DI 01-DEC-2001 (TrEMBLrel. 19, Created)
DI 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
DE P0434804.14 PROTEIN.
GN P0434804.14.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Cryzoa; Poaceae.
OX NCBI_TaxID:4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354012; PubMed 11447274;
RA Chiu H.T., Hubbard B.K., Shah A.N., Fiske J., Frodenberg K.A.,
RA Walsh C.T., Khosla C.;
RT "Molecular cloning and sequence analysis of the complexatin
RT biosynthetic gene cluster of Streptomyces lavendulae."
RL Proc. Natl. Acad. Sci. U.S.A. 98:8508-8554(2001).
RL EMBL: AF496507; AAK91433.1;
SEQUENCE 212 AA; 22582 MW; 77181AAB758D546 CR664;

Query Match          90.3%; Score 28; DB 19; Length 212;
Best Local Similarity 83.3%; Pred. No. 1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGGK 6
   1:|||||
DB 167 LQGGK 172

RESULT 14
Q914P2
ID Q914P2 PRELIMINARY; PRT; 245 AA.

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AC Q914P2;
DI 01-MAR-2001 (TREMblrel, 16, Created)
DI 01-MAR-2001 (TREMblrel, 16, Last sequence update)
DI 01-DEC-2001 (TREMblrel, 19, Last annotation update)
DE PROBABLE SHORT-CHAIN DEHYDROGENASE.
GN PA1470.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_taxID=287;
LN 111
SEQUENCE FROM N.A.
RP STRAIN:ATCC 15692 / PA01;
RX MEDLINE 2944733; PubMed:1098493;
RA Stover C.K., Pham X.-T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.L., Brennan P.S.L., Prinzing W.C., Kowalik D.L., Latham R.,
RA Garber E.L., Goffey L., Tolentino E., Westbrook Wadman S., Yuan Y.,
RA Brady L., Goffey S.N., Pelzer K.E., Kan A., Larkins E., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.L.,
RA Keizer J., Sailer M.H., Hancock K.E.W., Lory S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RA Nature 406:959-964(2000);
CC -; SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
OC (SD) FAMILY.
DR EMBL: AE004576; AAC04859.1; -.
DR BSSP: G12634; YBRV.
DR InterPro: IPR002198; A0H_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINIS: PR00080; SDHFAMILY.
KW Complete proteome; oxidoreductase.
SQ SEQUENCE 245 AA; 25365 MW; 342A1CE123A00744 CRC64;

Query Match 90.38; Score 28; 108 16; Length 245;
Best Local Similarity 83.38; Prod. No. 2.3e-02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQRGR 6
11111
DB 129 VQRGR 134

RESULT 15
Q927X9
AC Q927X9; PRELIMINARY; PRT; 283 AA.
DI 01-DEC-2001 (TREMblrel, 19, Created)
DI 01-DEC-2001 (TREMblrel, 19, Last sequence update)
DI 01-DEC-2001 (TREMblrel, 19, Last annotation update)
DE LIN2658 PROTEIN.
GN LIN2658.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.
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RA Madueno E., Maillot M., Mada Vicente J., Nt E., Nedjati R.,
RA Nordstedt G., Novella S., de Pablos R., Perez Diaz J.C., Purcell R.,
RA Roumel H., Rose M., Schluter T., Simoes N., Tiorrez A.,
RA Vazquez-Boland J.A., Voss H., Wehland J., Gassart P.;
RA "Comparative genomics of Listeria species.";
RA Science 294:849-852(2001).
EMBL: AL596173; CA597884.1; -.

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Le Test Blast: LIN2658;
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DB 129 VQRGR 134

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PT VIA-1 for treating inflammatory disorders, in particular arthritis
 XX Claim 1: Fig 15; 60pp; English.
 PS
 XX The present invention relates to the use of an alpha-helical domain
 CC blocking activity capable of blocking the proteolytic cleavage of human alpha
 CC integrin domain (VIA-1). The antibody of the present invention is
 CC useful for treating an inflammatory disorder e.g. rheumatoid arthritis,
 CC skin related conditions such as psoriasis, eczema, burns and dermatitis,
 CC asthma, bronchitis, menstrual cramps, tendinitis, bursitis, and the
 CC treatment of pain and headaches, or as an antipyretic, for the treatment
 CC of fever, gastrointestinal conditions such as inflammatory bowel
 CC diseases, Crohn's disease, gastritis and vascular diseases, migraine
 CC headaches, psoriasis, eczema, tendinitis, bursitis, dermatitis, Raynaud's
 CC disease, rheumatic fever, type 1 diabetes, myasthenia gravis, multiple
 CC sclerosis, sarcoidosis, nephrotic syndrome, myocardial ischemia,
 CC allergic rhinitis, respiratory distress syndrome, and acute shock
 CC syndrome and atherosclerosis.
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 CC Sequence 6 AA:
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 CC 04-DEC-2001 (first entry)
 CC DE
 CC Human novel extracellular matrix protein, 351 ID NO 281.
 CC XX
 CC Human secreted extracellular matrix protein, immunomodulatory.
 CC KW Anti-HIV; anti-oncogenic; antirheumatic; antischlerotic; cardiac; vascular;
 CC KW cerebroprotective; thrombolytic; antileukemic; opthalmic; cytostatic;
 CC FW anti-leukemia; immunomodulatory; HIV; HIV-1; HIV-2; HIV-3; HIV-4;
 CC FW human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;
 CC KW cancers; hyperproliferative disorder; breast neoplasia; melanoma;
 CC KW Secondary syphilis; leishmaniasis; leishmaniasis; leishmaniasis;
 CC KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
 CC KW cardiac arrest; tachycardia; angina; infarction; venous thrombosis;
 CC KW wound healing; immunogen; gene therapy; antileukemic; antischlerotic;
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RESULT 6

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111111
DB 91 VQ6GR 14

RESULT 7

AAU5764
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QY 1 VQ6GR 6
111111
DB 91 VQ6GR 96

RESULT 6

AAU47587
ID AAU47587 standard: Protein, 378 AA.

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QY 1 VQ6GR 6
111111
DB 91 VQ6GR 14

RESULT 7

AAU5764
ID AAU5764 standard: Protein, 755 AA.

XX AC

XX AC

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XX Crenarchaeum symbiosum: non-thermophilic; crenarchaeote; physiology;
 KW characterisation; archae; therapeutic; industrial; laboratory;
 XX Crenarchaeum symbiosum.

XX W0200018909-A2.

XX 06-APR-2000.

XX 29-SEP-1999; 9980-US22752.

XX 29-SEP-1999; 980S-0102294

XX (DIVE-) DIVERSA CORP.

XX Swanson RV, Feldman RA, Schleper C;

XX W01-2000-29219-07

XX N-PSDB; AAA55198.

XX New nucleic acids and proteins isolated from the non-thermophilic
 PT crenarchaeote Crenarchaeum symbiosum; useful in characterizing the
 PT physiology of these archae and in therapeutic, industrial or laboratory
 PT techniques
 XX Claim 26; Page 134; 210pp; English.

XX AAA55186 to AAA55226 and AAY90913 to AAY90951 represent nucleic acids
 CC and proteins isolated from the non-thermophilic crenarchaeote
 CC Crenarchaeum symbiosum. The nucleic acids and proteins identified in
 CC the present invention are useful in characterizing the physiology of
 CC these archae and can be used in therapeutic, industrial or laboratory
 CC techniques. AAA55227 to AAA55260 represent promoter sequences from
 CC Crenarchaeum symbiosum. AAA55261 to AAA55265 represent Fok primers and
 CC probes used in examples from the present invention.

XX Sequence 269 AA;

Query Match 96.8%; Score 30; DB 21; Length 269;

Best Local Similarity 83.9%; Pred. No. 9 8000;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGR 6

DB 55 TORGR 60

RESULT 11

AA90949

ID AAY90939 standard; Protein: 273 AA.

XX AC AAY90949;

XX 30-AUG-2000 (first entry)

XX Crenarchaeum symbiosum open reading frame Protein sequence SEQ ID NO:56.

XX Crenarchaeum symbiosum: non-thermophilic; crenarchaeote; physiology;

XX characterisation; archae, therapeutic; industrial; laboratory.

XX Crenarchaeum symbiosum.

XX W0200018909 A2.

XX 06-APR 2000

XX 29-SEP-1999; 9949-US22752.

XX 29-SEP-1999; 980S-0102294.

XX (DIVE-) DIVERSA CORP

XX Swanson RV, Feldman RA, Schleper C;

XX W01-2000-29219-25.

XX N-PSDB; AAA55214.

XX New nucleic acids and proteins isolated from the non-thermophilic
 PT crenarchaeote Crenarchaeum symbiosum; useful in characterizing the
 PT physiology of these archae and in therapeutic, industrial or laboratory
 PT techniques

XX Claim 26; Page 171; 210pp; English.

XX AAA55186 to AAA55226 and AAY90913 to AAY90951 represent nucleic acids
 CC and proteins isolated from the non-thermophilic crenarchaeote
 CC Crenarchaeum symbiosum. The nucleic acids and proteins identified in
 CC the present invention are useful in characterizing the physiology of
 CC these archae and can be used in therapeutic, industrial or laboratory
 CC techniques. AAA55227 to AAA55260 represent promoter sequences from
 CC Crenarchaeum symbiosum. AAA55261 to AAA55265 represent Fok primers and
 CC probes used in examples from the present invention.

XX Sequence 273 AA;

Query Match 96.8%; Score 30; DB 21; Length 273;

Best Local Similarity 83.9%; Pred. No. 2 8000;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGR 6

DB 59 TORGR 64

RESULT 12

ABB16230

ID ABB16230 standard; Protein: 64 AA.

XX AC ABB16230;

XX 23-JAN-2002 (first entry)

XX Human nervous system related polypeptide (23-10-90 4997.

XX Human; neurotropic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnerary;
 KW antiparkinsonian; antischizoid; antidiabetic; antitumor; cancer;
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
 KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine.

XX Homo sapiens.

XX W020015936; A2.

XX 16-AUG-2001.

XX 17 JAN 2001. 2001W0 0301334.

XX 11 JAN 2000; 2000W0 0179045.

XX 04-DEC-2000; 2000W0 0180638.

XX 24-FEB-2000; 2000W0 0184664.

XX 02-MAR-2000; 2000W0 0186350.

XX 16-MAR-2000; 2000W0 0189874.

XX 17-MAR-2000; 2000W0 0190076.

XX 18-APR-2000; 2000W0 0198124.

XX 19-MAY-2000; 2000W0 0205515.

XX 07-JUN-2000; 2000W0 0205467.

XX 28-JUN-2000; 2000W0 0214886.

XX 30-JUN-2000; 2000W0 0215145.

XX 07-JUL-2000; 2000W0 0216647.

XX 07-JUL-2000; 2000W0 0216880.

XX 11-JUL-2000; 2000W0 0217187.

XX 11-JUL-2000; 2000W0 0217496.

XX 14-JUL-2000; 2000W0 0218290.

CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at http://wipo.int/pub/published_pct_sequences.

XX Sequence 64 AA;

Query Match: 90.38; Score 28; Db 9; Length 64;

Best Local Similarity 83.38; Pred. No. 1.8e+02;

Matches 5; Conservative 1; Mismatches 9; Indels 0; Gaps 0.

Q7 1 VQVGRP 6

Db 18 VERGRF 24

RESULT 13

AAP81759

ID AAP81759 standard; protein; 145 AA.

XX

AC AAP81759.

XX

PT 15-NOV-1990 (first entry)

XX Sequence encoded by env gene of HIV-1 (continued from p81758).

XX AIDS; immunogen; antigen; vaccine; diagnostic.

XX Simian immunodeficiency virus.

XX W08805440-A.

XX

PN 28-JUL-1988.

XX

PD 15 JAN-1989; 89W-PE00025.

XX

PR 15-APR-1987; 87EW-0005398

XX

XX (INSP) INST PASTER(A117.7)

XX

PA Allison M, Montagnier L, Ghetard B, Clavel F, Sonigo P, Guyader M;

PI Tilotais P, Chakrabarti L, Destosiens R;

XX

XX WPI: 1988-220290/41.

XX

XX N-PSDB; AAN80860.

XX

PT New peptides with immunological properties of HIV-2 envelope protein -
 PT having the structure of simian immune deficiency virus proteins,
 PT useful in diagnosis and of vaccine components

XX Disclosure: Fig 1b; 86pp; French.

XX

CC New peptides which have immunological properties in common with those of
 CC the peptide skeleton of the envelope protein of HIV 2 and also have a
 CC peptide structure in common with that of HIV-1 glycoprotein are claimed.
 CC Antigenic and immunogenic conjugates contain the peptides and a kit to
 CC detect HIV-2 in biological fluids are new. The peptides are useful for in
 CC vitro diagnosis of HIV-2 infection and some of them can be used as
 CC components of immunogenes and vaccines against HIV. Antisera raised
 CC against them can be used for treatment of AIDS.

XX Sequence 145 AA;

Query Match: 90.48; Score 28; Db 9; Length 145;

Best Local Similarity 83.38; Pred. No. 2.9e+02;

Matches 5; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 VQVGRG 6

Db 122 LQVGR 127

RESULT 14

AAY01198

ID AAY01198 standard; Protein; 212 AA.

XX

AC AAY01198;

XX

DI 18-MAY-1999 (first entry)

XX Polypeptide fragment encoded by gene 16.

XX Human secreted protein, gene therapy, protein therapy, tissue, cancer;
 XX tumor; neurodegenerative disorder; leukaemia; autoimmune disease; AIDS;
 XX developmental abnormality; fetal deficiency; Alzheimer's disease;
 XX cognitive disorder; schizophrenia; immunological disorder; mood disorder;
 XX immune deficiency disease; respiratory disorder; arthritis; skeletal;
 XX haematopoietic disorder; neural osteoporosis; metabolic disorders;
 XX cardiovascular; endocrine; gastrointestinal; asthma; diagnosis.

XX Homo sapiens.

XX W09901028 A2.

XX

PD 14 JAN-1999.

XX

PP 40-JUN-1998; 98WO US14608.

XX

PR 12-SEP-1997; 97US-0058663.

XX

PR 01-JUL-1997; 97US-0051481.

XX

PR 01-JUL-1997; 97US-0051480.

XX

PR 12-SEP-1997; 97US-0058598.

XX

XX (USMA) HUMAN GENOME SCI INC.

XX

XX Carter KC, Indress GA, Fama P, Rosen CA, Kelen SM;

XX WPI: 1999-105692/09.

XX

XX N-PSDB; AAX22126.

XX

PT New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of such diseases, neurological
 PT disorders, immune diseases, immune deficiency diseases or blood
 PT disorders

XX Disclosure: Page 27; 17pp; English.

XX

CC The invention relates to nucleic acid sequences (AAX22111 to AAX22144)
 CC encoding human secreted proteins (AAY01135 to AAY01158). The secreted
 CC protein gene sequences are deposited with the ATCC under deposit number
 CC ATCC 20419. Host cells comprising recombinant vectors containing the
 CC nucleic acid sequences are used for the recombinant production of the
 CC secreted proteins. The polynucleotide and amino acid sequences are useful
 CC for are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Pathological conditions can
 CC be also diagnosed by determining the amount of the new polypeptides in a
 CC sample or by determining the presence of mutations in the new
 CC polynucleotides. Specific uses are described for each of the
 CC polypeptides. Based on which tissues they are most highly expressed
 CC in, and include developing products for the diagnosis or treatment of
 CC cancer, tumours, developmental abnormalities and foetal deficiencies,
 CC autoimmune diseases, lymphomas, Alzheimer's and cognitive disorders,
 CC schizophrenia, immunological disorders, immune deficiency diseases,
 CC (AIDS), mood disorders, respiratory disorders, arthritis, asthma,
 CC haematopoietic disorders, neural disorders, skeletal disorders,
 CC osteoporosis, metabolic disorders, cardiovascular disorders, endocrine
 CC disorders or gastrointestinal disorders. The polypeptides are also useful
 CC for identifying their binding partners. The present sequence represents a
 CC polypeptide fragment encoded by a gene of the invention (see description;
 CC line for gene number).

XX Sequence 212 AA;

Query Match:

90.48; Score 28; Db 20; Length 212;



TELECOMMUNICATION INFORMATION:

TELEPHONE: (404) 864-9700
 TELEFAX: (404) 864-0224
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1065 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09 640-172-9

Query Match 87.1% Score 277 BB 47 Length 1065
 Best Local Similarity 100.0% Pred. No. 10-04
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QRGGR 6

DB 465 QRGGR 469

RESULT 6

US 09 475-419 9
 Sequence 9, Application US/09/475419
 Patent No. 624950

GENERAL INFORMATION:

APPLICANT: SHARFZ, Uwe
 TITLE OF INVENTION: NOVEL PROTEIN AND PROTEIN FOR 1
 TITLE OF INVENTION: LYMPH CYCLE VEGF
 NUMBER OF SEQUENCES: 41
 CORRESPONDENCE ADDRESS:
 ADDRESS: Sheridan Pass 5 Mcintosh
 STREET: 1700 Lincoln Street, 35th Floor
 CITY: Denver
 STATE: Colorado
 COUNTRY: U.S.
 ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/475,419
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION NUMBER: 08/640,172
 FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Connolly, Gary J.
 REGISTRATION NUMBER: 32 020
 REFERENCE/SECRET NUMBER: 2879-36
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 864-9700
 TELEFAX: (404) 864-0224

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1065 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US 09 475-419 9

Query Match 97.1% Score 277 BB 47 Length 1065
 Best Local Similarity 100.0% Pred. No. 10-04
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QRGGR 6

DB 465 QRGGR 469

RESULT 7

US 09 475-419 2

Sequence 9, Application US/09/475419
 Patent No. 624950

GENERAL INFORMATION:

APPLICANT: Benoit, Stephen H.
 APPLICANT: Shaban, Terina
 APPLICANT: Chao, Maria
 APPLICANT: Elliott, Scott
 TITLE OF INVENTION: CANALYTIK 1 PEPTIDES FOR INDUCTION
 TITLE OF INVENTION: PROLINE TELARGES
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESS: BEVY, WILLIAMS, TIMMONS & COLLINS
 STREET: 1101 Walnut St.
 CITY: Kansas City
 STATE: Mo
 COUNTRY: USA
 ZIP: 64106

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/475,419
 FILING DATE: 03-SEP-1997
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/229,513
 FILING DATE: 19 APR 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Collins, John M.
 REGISTRATION NUMBER: 26262
 REFERENCE/SECRET NUMBER: 22844
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (816) 474-9050
 TELEFAX: (816) 474-9057
 TELEX: 44 463

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1170 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: No
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 CELL TYPE: T cell
 CELL LINE: HL-60
 FEATURE:
 NAME/KEY: location
 LOCATION: 1-25
 OTHER INFORMATION: /label signal
 OTHER INFORMATION: /note "Signal sequence"
 FEATURE:
 NAME/KEY: location
 LOCATION: 42-179
 OTHER INFORMATION: /label Repeat
 OTHER INFORMATION: /note "Repeat 1"
 FEATURE:
 NAME/KEY: location
 LOCATION: 82-132
 OTHER INFORMATION: /label Repeat
 OTHER INFORMATION: /note "Repeat 11"
 FEATURE:
 NAME/KEY: location
 LOCATION: 329-391
 OTHER INFORMATION: /label Repeat
 OTHER INFORMATION: /note "Repeat 111"
 FEATURE:
 NAME/KEY: location
 LOCATION: 392-446
 OTHER INFORMATION: /label Repeat

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1  OTHER INFORMATION: /note= "Repeat IV"
2  FEATURE:
3  NAME/KEY: Region
4  LOCATION: 417..538
5  OTHER INFORMATION: /label= Repeat
6  OTHER INFORMATION: /note= "Repeat V"
7  FEATURE:
8  NAME/KEY: Region
9  LOCATION: 509..567
10 OTHER INFORMATION: /label= Repeat
11 OTHER INFORMATION: /note= "Repeat VI"
12 FEATURE:
13 NAME/KEY: Region
14 LOCATION: 568..629
15 OTHER INFORMATION: /label= Repeat
16 OTHER INFORMATION: /note= "Repeat VII"
17 FEATURE:
18 NAME/KEY: Domain
19 LOCATION: 1089..1112
20 OTHER INFORMATION: /label= Trans
21 OTHER INFORMATION: /note= "Transmembrane Domain"
22 FEATURE:
23 NAME/KEY: Domain
24 LOCATION: 1113..1170
25 OTHER INFORMATION: /label= Cyt
26 OTHER INFORMATION: /note= "Cytoplasmic domain"
27 PUBLICATION INFORMATION:
28 AUTHORS: Pigott,
29 TITLE: LFA-1 Amino acid sequence (alpha) (from
30 JOURNAL: PMA-stimulated HL-60 cells)
31 PAGES: 94-95
32 DATE: 1993
33 RELEVANT RESIDUES IN SEQ ID NO: 2: 168H 1 14-1170
34
35 US-08-789 078-2
36
37 Query Match 87.1%; Score 27; DB 2; Length 1170;
38 Best local similarity 100.0%; Pred. No. 1, Rev 3;
39 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
40
41 2 QUORR 6
42 1111
43 1b 489 QUORR 453
44
45 RESULT 8
46 US-08-752-633-2
47 Sequence 2: Application 02/08/950202
48 Patent No. 6663886
49 GENERAL INFORMATION:
50 APPLICANT: Benedikt, Stephen H.
51 APPLICANT: Shaham, Iruma
52 APPLICANT: Chan, Maria
53 APPLICANT: Tibbitts, Scott
54 TITLE OF INVENTION: ICAM-1/CD-11c PEPTIDES FOR INDUCING
55 NUMBER OF SEQUENCES: 19
56 CORRESPONDENCE ADDRESS:
57 ADDRESSEE: ROY, WILLIAM, 1100-03 & C LLC
58 STREET: 1101 Walnut St.
59 CITY: Kansas City
60 STATE: MO
61 COUNTRY: USA
62 ZIP: 64106
63 COMPUTER READABLE FORM:
64 MEDIUM TYPE: Floppy disk
65 COMPUTER: IBM PC compatible

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1  OPERATING SYSTEM: PC-NT/MS-DOS
2  SOFTWARE: Patent In Release #1.0, Version #1.25
3  CURRENT APPLICATION DATA:
4  APPLICATION NUMBER: 05/0875202
5  FILING DATE:
6  CLASSIFICATION: 514
7  ATTORNEY/AGENT INFORMATION:
8  NAME: Collins, John M.
9  REGISTRATION NUMBER: 25262
10 REGISTRATION FIRM NUMBER: 22004
11 TELECOMMUNICATIONS INFORMATION:
12 TELEPHONE: (816)474-9050
13 TELEFAX: 816)474-9057
14 TELEX: 434-363
15 INFORMATION FOR SEQ ID NO: 2:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 1170 amino acids
18 TYPE: amino acid
19 TOPLOGY: linear
20 MOLECULE TYPE: protein
21 HYPOTHEICAL: NO
22 ORIGINAL SOURCE:
23 ORGANISM: Homo sapiens
24 CELL TYPE: T cell
25 CELL LINE: HL-60
26 FEATURE:
27 NAME/KEY: Region
28 LOCATION: 1..25
29 OTHER INFORMATION: /label= signal
30 OTHER INFORMATION: /note= "Signal sequence"
31 FEATURE:
32 NAME/KEY: Region
33 LOCATION: 32..79
34 OTHER INFORMATION: /label= Repeat
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36 FEATURE:
37 NAME/KEY: Region
38 LOCATION: 82..142
39 OTHER INFORMATION: /label= Repeat
40 OTHER INFORMATION: /note= "Repeat II"
41 FEATURE:
42 NAME/KEY: Region
43 LOCATION: 492..446
44 OTHER INFORMATION: /label= Repeat
45 OTHER INFORMATION: /note= "Repeat IV"
46 FEATURE:
47 NAME/KEY: Region
48 LOCATION: 447..508
49 OTHER INFORMATION: /label= Repeat
50 OTHER INFORMATION: /note= "Repeat V"
51 FEATURE:
52 NAME/KEY: Region
53 LOCATION: 509..567
54 OTHER INFORMATION: /label= Repeat
55 OTHER INFORMATION: /note= "Repeat VI"
56 FEATURE:
57 NAME/KEY: Region
58 LOCATION: 568..629
59 OTHER INFORMATION: /label= Repeat
60 OTHER INFORMATION: /note= "Repeat VII"
61 FEATURE:
62 NAME/KEY: Domain
63 LOCATION: 170..309
64 OTHER INFORMATION: /label= Domain
65 OTHER INFORMATION: /note= "1-Domain"
66 FEATURE:
67 NAME/KEY: Domain
68 LOCATION: 1089..1112

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1 OTHER INFORMATION: /Label Trans
 2 OTHER INFORMATION: /note "Transmembrane domain"
 3 FEATURE:
 4 NAME/KEY: Domain
 5 LOCATION: 1113..1170
 6 OTHER INFORMATION: /Label Cyto
 7 OTHER INFORMATION: /note "Cytoplasmic domain"
 8 PUBLICATION INFORMATION:
 9 AUTHORS: Plooff,
 10 TITLE: LEA-1 Amino acid sequence (alpha1) (from
 11 TITLE: PMA-stimulated HL-60 cells)
 12 JOURNAL: The Adhesion Molecule Facts Book
 13 PAGES: 94-95
 14 DATE: 1994
 15 RELEVANT REFERENCES IN SEQ ID NO: 2 FROM 1 TO 1170
 16 US 08-752-533-2

Query Match 87.1%, Score 27, DB 2, Length 1170,
 Best Local Similarity 100.0%, Prod. No. 1,1e+04,
 Matches 5, Conservative 0, Mismatches 0, Models 0,

QY 2 gb03R 6
 1111
 DB 489 QRCR 494

RESULT 9
 US-08-476-062A-42
 1 Sequence 42, Application US/08476062A
 2 Patent No. 5877275
 3 GENERAL INFORMATION:
 4 APPLICANT: Alnaut, M. Amin
 5 TITLE OF INVENTION: CONTROLLING CELLULAR RESPONSE/INFLUENCE BY
 6 TITLE OF INVENTION: RESPONSES WITH RETAL INTEGRINS
 7 NUMBER OF SEQUENCES: 53
 8 CORRESPONDENCE ADDRESS:
 9 ADDRESSEE: Fish & Richardson P.C.
 10 STREET: 225 Franklin Street
 11 CITY: Boston
 12 STATE: MA
 13 COUNTRY: US
 14 ZIP: 02110-2884
 15 COMPUTER READABLE FORM:
 16 MEDIUM TYPE: Diskette
 17 COMPUTER: IBM compatible
 18 OPERATING SYSTEM: Windows95
 19 SOFTWARE: FASTSEQ for Windows Version 2.0
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: US/08/476-062A
 22 FILING DATE: 07-JUN-1995
 23 PRIOR APPLICATION DATA:
 24 APPLICATION NUMBER: 08/216,081
 25 FILING DATE: 21-MAR-1994
 26 APPLICATION NUMBER: 07/547,830
 27 FILING DATE: 04-JAN-1991
 28 APPLICATION NUMBER: 07/549,842
 29 FILING DATE: 18-JUN-1990
 30 APPLICATION NUMBER: 07/212,574
 31 FILING DATE: 28-JUN-1988
 32 ATTORNEY/AGENT INFORMATION:
 33 NAME: Freedman, John W.
 34 REGISTRATION NUMBER: 29,066
 35 REFERENCE/AGENT NUMBER: 372,322
 36 TELECOMMUNICATION INFORMATION:
 37 TELEPHONE: 617/445-5570
 38 TELEFAX: 617/542-8906
 39 TELEX: 289154
 40 INFORMATION FOR SEQ ID NO: 42:
 41 SEQUENCE CHARACTERISTICS:
 42 LENGTH: 1170 amino acids
 43 TYPE: amino acid
 44 TOPOLOGY: Linear

1 MOLECULE TYPE: Protein
 2 EXAMINER TYPE: Internal
 3 US 08-476-062A-42
 4 Query Match 87.1%, Score 27, DB 2, Length 1170,
 5 Best Local Similarity 100.0%, Prod. No. 1,1e+04,
 6 Matches 5, Conservative 0, Mismatches 0, Models 0,
 7 QY 2 gb03R 6
 8 1111
 9 DB 489 QRCR 494
 10 RESULT 10
 11 PCT US95-04886-2
 12 PCT APPLICATION NO. 17/US9504886
 13 GENERAL INFORMATION:
 14 APPLICANT: Reedner, Stephen B.
 15 APPLICANT: Stabaud, Bernard
 16 APPLICANT: Chan, Marcia
 17 APPLICANT: Edwards, Scott
 18 TITLE OF INVENTION: LEA-1/LEA-1 PEPTIDES FOR INHIBITIN
 19 TITLE OF INVENTION: IMMUNE TOLERANCE
 20 NUMBER OF SEQUENCES: 19
 21 CORRESPONDENCE ADDRESS:
 22 ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
 23 STREET: 1101 Walnut St.
 24 CITY: Kansas City
 25 STATE: Mo
 26 COUNTRY: USA
 27 ZIP: 64106
 28 COMPUTER READABLE FORM:
 29 MEDIUM TYPE: Floppy disk
 30 SOFTWARE: IBM PC compatible
 31 CREATING SYSTEM: PC-5/MS DOS
 32 SOFTWARE: Patent to Release #1.0, Version #1.25
 33 CURRENT APPLICATION DATA:
 34 APPLICATION NUMBER: PCT/US95/04886
 35 FILING DATE:
 36 CLASSIFICATION:
 37 ATTORNEY/AGENT INFORMATION:
 38 NAME: Collins, John M.
 39 REGISTRATION NUMBER: 26262
 40 REFERENCE/AGENT NUMBER: 22844
 41 FILING DATE: 08/04/95
 42 TELEPHONE: (816)474-9050
 43 TELEFAX: 816/474-9057
 44 TELEX: 44 563
 45 INFORMATION FOR SEQ ID NO: 2:
 46 SEQUENCE CHARACTERISTICS:
 47 LENGTH: 1170 amino acids
 48 TYPE: amino acid
 49 TOPOLOGY: Linear
 50 MOLECULE TYPE: protein
 51 HYDROPHILIC: NO
 52 ORIGINAL SOURCE:
 53 ORGANISM: Homo Sapiens
 54 CELL TYPE: T cell
 55 CELL LINE: HL-60
 56 FEATURE:
 57 SOURCE: Isolation
 58 LOCATION: 1..25
 59 OTHER INFORMATION: /Label Signal
 60 /note "Signal sequence"
 61 FEATURE:
 62 NAME/KEY: Isolation
 63 LOCATION: 42..79
 64 OTHER INFORMATION: /Label Repeat
 65 /note "Repeat 1"
 66 FEATURE:
 67 NAME/KEY: Isolation
 68 LOCATION: 84..142
 69 OTHER INFORMATION: /Label Repeat

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OTHER INFORMATION: /note "Repeat 11"
FEATURE:
NAME/KEY: Feature
LOCATION: 399,1291
OTHER INFORMATION: /label Repeat
OTHER INFORMATION: /note "Repeat 11"
FEATURE:
NAME/KEY: Region
LOCATION: 392,1446
OTHER INFORMATION: /label Repeat
OTHER INFORMATION: /note "Repeat 1V"
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NAME/KEY: Region
LOCATION: 447,1508
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OTHER INFORMATION: /note "Repeat V"
FEATURE:
NAME/KEY: Region
LOCATION: 509,1567
OTHER INFORMATION: /label Repeat
OTHER INFORMATION: /note "Repeat V1"
FEATURE:
NAME/KEY: Region
LOCATION: 568,1629
OTHER INFORMATION: /label Repeat
OTHER INFORMATION: /note "Repeat VII"
FEATURE:
NAME/KEY: Domain
LOCATION: 170,1349
OTHER INFORMATION: /label Domain
OTHER INFORMATION: /note "I-Domain"
FEATURE:
NAME/KEY: Domain
LOCATION: 1089,1112
OTHER INFORMATION: /label Trans
OTHER INFORMATION: /note "Transmembrane domain"
FEATURE:
NAME/KEY: Domain
LOCATION: 1113,1170
OTHER INFORMATION: /label Cyto
OTHER INFORMATION: /note "Cytoplasmic domain"
PUBLICATION INFORMATION:
AUTHORS: Pliott,
TITLE: LEA-1 Amino acid sequence (alpha) (from
JOURNAL: The Adhesion Molecule Facts Book
PAGES: 94-95
DATE: 1993
RELEVANT RESIDUES IN SEQ ID NO: 2, FROM 1 TO 1170
PCT-US96-04886-2

Query Match 87.1% Score 27; DB 5; Length 1170;
Best Local Similarity 100.0%; Pred. No. 1,1e+03;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 2 ORIGIN 6
DB 489 ORIGIN 493

RESULT 11
PCT-US96-01314-42
Sequence 42 Application PCT/US9601314
GENERAL INFORMATION:
APPLICANT: M. Amin Ahnaut
TITLE OF INVENTION: ANTAGONISTS FOR IDENTIFYING INTERFERON
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: BOSTON

```

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STATE: Massachusetts
COUNTRY: U.S.A.
CIF: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
S.M.B.I.R.: IBM PC, MS-DOS 5.0
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,167
FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
FAX: (617) 542-8506
TELEX: 200154
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 1170
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: Linear
PCT-US96-01414-42

Query Match 87.1% Score 27; DB 5; Length 1170;
Best Local Similarity 100.0%; Pred. No. 1,1e+03;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 2 ORIGIN 6
DB 489 ORIGIN 493

RESULT 12
US-09-144-085-1
Sequence 1 Application US/99144085
Patent No. 6280999
GENERAL INFORMATION:
APPLICANT: Gustafsson, Claes
APPLICANT: Bellach, Mary C.
APPLICANT: Ashley, Gary
APPLICANT: Julien, Bryan
APPLICANT: Ziermann, Rainer
TITLE OF INVENTION: ORGANISM POLYMERIZABLE SYNTHESIS AND EXPANDING DNA
FILE REFERENCE: 1996020020-20
CURRENT APPLICATION NUMBER: US/99/144,085
CURRENT FILING DATE: 1998-08-31
EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 1
LENGTH: 5087
TYPE: PRT
ORGANISM: Soranidium cellulosum
US-09-144-085-1

Query Match 87.1% Score 27; DB 4; Length 5087;
Best Local Similarity 83.4%; Pred. No. 4,6e+03;
Matches 5; Conservative 1; Mismatches 0; Gaps 0;

QY 1 ORIGIN 6
DB 2846 ORIGIN 2841

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RESULT 13

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US-09-144-085-2
; Sequence 2: Application US/09/144085
; Patent No. 6280999
; GENERAL INFORMATION:
; APPLICANT: Gustafsson, Claes
; APPLICANT: Botlach, Gary C.
; APPLICANT: Ashley, Gary
; APPLICANT: Jullien, Bryan
; APPLICANT: Ziemann, Rainer
; TITLE OF INVENTION: OVERLAPPING POLYMERIZATION AND IMPRINTING DATA
; FILE REFERENCE: 30962-20020-29
; CURRENT APPLICATION NUMBER: 09/09/144,085
; CURRENT FILING DATE: 1998-08-31
; EARLIER APPLICATION NUMBER: 09/010,809
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6095
; TYPE: PRT
; ORGANISM: Soranidium cellulosum
US-09-144-085-2

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Query Match      87.1%; Score 27; DB 4; Length 6095;
Best Local Similarity 83.4%; Prod. No. 5,500,04;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VOR68R 6
11111
DB 2954 VRR63R 2959

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RESULT 14

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US-09-564-805-233
; Sequence 233: Application US/09/564805
; Patent No. 6333503
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p Linked Prostate Cancer Susceptibility
; FILE REFERENCE: 2418-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/444,482
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 233
; LENGTH: 684
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-805-233

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Query Match      83.9%; Score 26; DB 4; Length 684;
Best Local Similarity 83.3%; Prod. No. 1,200,04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 VOR68R 6
11111
DB 240 VRR63R 235

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RESULT 15

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US-09-564-805-235
; Sequence 235: Application US/09/564805

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; Patent No. 6333503
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and orthologous genes
; FILE REFERENCE: 2418-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 09/444,482
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/444,482
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 235
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-564-805-235

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Query Match      83.9%; Score 26; DB 4; Length 779;
Best Local Similarity 83.4%; Prod. No. 1,200,04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 VOR68R 6
11111
DB 235 VRR63R 240

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Search completed: October 22, 2002, 16:02:44
Job Time: 2:00:57.000

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